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From: Nickol, Gary
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AUG 12 2003 8/13 43

8/14 171

(STIC) 8/15 135

8/18 76

8/19 61

8/20 6

Please search and interference search the following:

SEQ ID NO:41

Thanks,

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Point of Contact:
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Technical Info. Specialist
CM1 6A04
703-308-3534

41-2456 na

Searcher: _____
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TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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Other (specify): _____

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 11:41:37 ; Search time 8705 Seconds
(without alignments)
11542.107 Million cell updates/sec

Title: US-10-021-660-41

Perfect score: 2456

Sequence: 1 gcaagcacggaacaagctga.....aatgtgaaaaaaaaccg 2456

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

7: gb.pl.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: em.ba.*

15: em.fun.*

16: em.in.*

17: em.mu.*

18: em.ov.*

19: em.ph.*

20: em.pl.*

21: em.ro.*

22: em.sts.*

23: em.un.*

24: em.vi.*

25: em.htg_hum.*

26: em.htg_inv.*

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28: em.htg_pln.*

29: em.htg_rod.*

30: em.htg_mam.*

31: em.htg_vrt.*

32: em_sy.*

33: em_higo_hum.*

34: em_higo_mus.*

35: em_higo_pln.*

36: em_higo_rod.*

37: em_higo_mam.*

38: em_higo_vrt.*

39: em_higo_sy.*

40: em_higo_pln.*

41: em_higo_rod.*

42: em_higo_mam.*

43: em_higo_vrt.*

44: em_higo_sy.*

45: em_higo_pln.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2456	100.0	2456	6	AR270913
2	2456	100.0	2456	9	HSBMXGENE
3	2424.4	98.7	2449	6	AX244661
4	2404.2	97.9	2604	9	AF045459
5	2397.6	97.6	2500	6	AR179663
6	2397.6	97.6	2500	6	AR274488
7	2393.2	97.4	2553	9	BC016652
8	1641.8	66.8	2609	10	MMU88091
9	1639.6	66.8	2369	10	AF012104
10	494.6	20.1	2468	6	AX718901
11	494.6	20.1	2468	6	MUSBTACDNA
12	494.6	20.1	2493	10	BC053392
13	493	20.1	2485	10	MUSBPX
14	493	20.1	2505	6	I25434
15	485	19.7	1365	6	AX467404
16	485	19.7	2560	6	AX718899
17	485	19.7	2560	9	HSATK
18	480.2	19.6	2546	10	MUSEMBX
19	447.6	18.2	2162	5	REU85659
20	440.4	17.9	159446	9	AC003669
21	440.4	17.9	194492	9	AC097625
22	439.4	17.9	2574	6	AR148881
23	439.4	17.9	2574	6	AR270952
24	436	17.8	1971	5	AF535118
25	433.6	17.7	2574	10	S53716
26	433.6	17.6	2598	10	BC037071
27	433	17.5	2564	9	HMTYRKINA
28	430.2	17.5	2578	10	HMTYRKINA
29	429.8	17.5	2578	10	HMTYRKINA
30	421.2	17.1	2255	10	AF285881
31	409	16.7	1680	10	MMU19607
32	409	16.7	2204	10	MMU16145
33	409	16.7	2221	10	MUSRLK
34	409	16.7	2282	10	D83201
35	409	16.7	2342	10	MUSPTKRL18
36	409	16.7	2445	10	D83202
37	398.4	16.2	4224	10	MUSLTK
38	396.8	16.2	1878	6	AX695694
39	396.8	16.2	4231	10	MUSTYRKIN
40	396.8	16.2	4294	6	AX695693
41	396.8	16.2	4294	10	MUSITKA
42	392.8	16.0	3650	9	HUMPTKA
43	392	16.0	2480	10	MUSEMTX
44	388	15.8	3593	6	AX244656
45	385.4	15.7	1368	6	AX467388

ALIGNMENTS

RESULT 1	AR270913	2456 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR270913	Sequence 1476 from patent US 6500938.			
DEFINITION	AR270913	Sequence 1476 from patent US 6500938.			
ACCESSION	AR270913	GI:29702147			
VERSION	AR270913.1				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2456)				
AUTHORS	Au-Young, J. and Seilhamer, J.J.				
TITLE	Composition for the detection of signaling pathway gene expression				
JOURNAL	Patent: US 6500938-A 1476 31-DEC-2002;				
FEATURES	Location/Qualifiers				

Pred. No. is the number of results predicted by chance to have a

QY 841 CACACCCTCAAAAGATTTTCATGGAAATCCCTGAGTCAAGTTCATCTGAAGAAAGAGAA 900
Db 841 CACACCCTCAAAAGATTTTCATGGAAATCCCTGAGTCAAGTTCATCTGAAGAAAGAGAA 900
QY 901 AACCTGATGATATGACTGGTTGCTGGTAAACATCTCCAGATCACAAATCTGACAGTTA 960
Db 901 AACCTGATGATATGACTGGTTGCTGGTAAACATCTCCAGATCACAAATCTGACAGTTA 960
QY 961 CTCAGACAAAGGAAAGAGAGCATTTATGTTAGAAATTCGACCAAGTGGGAATG 1020
Db 961 CTCAGACAAAGGAAAGAGAGCATTTATGTTAGAAATTCGACCAAGTGGGAATG 1020
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Db 1021 TACACAGTCTCTTATTTAGTAAAGCTGTGAATGATAAAAGAACTGTCAAAACATATC 1080
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QY 1501 GATATATAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
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QY 1741 GTCGGAACAAAGTTTCCAGTCAAGTGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
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Db 1801 AGCAGCAAGTCAAGCTATGGGCAATTTGGGATCTGATGTTGGGAGGTGTTTCCAGCTGGGG 1860
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Db 1921 AGGCTTTACGGGGCCCCACCTGGCATCGGACACCATCTACCATGATCATGTACAGCTGCTGG 1980
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Db 2041 CGGAAAAGCAAGCATTGAAAGAAATTTAGGAGTCTGATAAGATGATATAGATG 2100
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Db 2161 TTTTAAATAGTCT 2220
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QY 2401 ATTTGTCAACAAATTTAAATATATCTACCAAGTACAGAAATTTGGAAGGCAAAACCG 2456
Db 2401 ATTTGTCAACAAATTTAAATATATCTACCAAGTACAGAAATTTGGAAGGCAAAACCG 2456

RESULT 3
LOCUS AX244661 2449 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 11 from Patent WO0166107.
ACCESSION AX244661
VERSION AX244661.1 GI:15859547
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Foxwell,B.M.
TITLE Treatment of diseases associated with cytokine production with inhibitors of the tec family of protein tyrosine kinases
JOURNAL Patent: WO 0166107-A 11 13-SEP-2001;
FEATURES THE MATHILDA AND TERENCE KENNEDY INSTITUTE OF RHEUMATOLOGY (GB)
Location/Qualifiers
1. 2449
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 797 a 495 c 548 g 609 t
ORIGIN

Query Match 98.7%; Score 2424.4; DB 6; Length 2449;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2439; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 GCAAGCAGGAAACAGCTGAGCGGATGATATATGGATACAAATCTATTCTAGAGAA 60
Db 1 GCAAGCAGGAAACAGCTGAGCGGATGATATATGGATACAAATCTATTCTAGAGAA 60
QY 61 CTTCTTCTCAAAAGATCACCAAAAGAAAGAAATGTCACCAATATATTTACAAAGCGG 120
Db 61 CTTCTTCTCAAAAGATCACCAAAAGAAAGAAATGTCACCAATATATTTACAAAGCGG 120

QY 121 CTTTTGTTTACCAAAACAACTTCTCTACTATGAATATGACAAATGAAAGGGC 180
DB 121 CTTTTGTTTACCAAAACAACTTCTCTACTATGAATATGACAAATGAAAGGGC 180
QY 181 AGCAGAAAGGATCCATTGAATTAAGAAATCAGATGTGGGAAAGTAAATCTCGAG 240
DB 181 AGCAGAAAGGATCCATTGAATTAAGAAATCAGATGTGGGAAAGTAAATCTCGAG 240
QY 241 GAGCAGACCCCTGTAGACAGACAGTACCATTTCAGATTGCTATAAAGATGGGCTTCTC 300
DB 241 GAGCAGACCCCTGTAGACAGACAGTACCATTTCAGATTGCTATAAAGATGGGCTTCTC 300
QY 301 TATGCTATGTCATCAATTAAGAGAGCCGAAAGTCAAGTGTGCAAGCAATTAACAAAAGAG 360
DB 301 TATGCTATGTCATCAATTAAGAGAGCCGAAAGTCAAGTGTGCAAGCAATTAACAAAAGAG 360
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DB 361 ATAAGGGGTACCCCTGCTGTCAGTCAAGTACCATAGTGGTTCCTGTCGACGGGAAG 420
QY 421 TTCCTGTGTTCCAGCAGAGCTGTAAGCAGCCCGAGGATGTACCCTCTGGGAACATAT 480
DB 421 TTCCTGTGTTCCAGCAGAGCTGTAAGCAGCCCGAGGATGTACCCTCTGGGAACATAT 480
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DB 781 AAAAGTAGCAGCAGTGAAGATGTGCAAGCAGTAACCAAAAGAAAGAAATGTGAAT 840
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DB 901 AACCTGGATGATTATGACTGGTGGTGAACATCTCCAGATCACAATCTGAACAGTTA 960
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DB 961 CTCAGACAAAGGAAAGAGAGCATTTATGTTAGAAATTCGAGCCAAAGTGGGAATG 1020
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DB 1021 TACACAGTGTCTTATTTAGTGAAGCTGTGAATGATAAAGGAAGCACTGCAAAACATATC 1080
QY 1081 CACGTGCATCAAAATGCTGAGACAAATATACCTGGCAGAAAACACTACTGTTTGAATTC 1140
DB 1081 CACGTGCATCAAAATGCTGAGACAAATATACCTGGCAGAAAACACTACTGTTTGAATTC 1140
QY 1141 ATTCCAAAGCTTATTCATATCATCAACAAATTCACAGAGCATATGATCACAGGCTCCGC 1200
DB 1141 ATTCCAAAGCTTATTCATATCATCAACAAATTCACAGAGCATATGATCACAGGCTCCGC 1200
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QY 1261 TGGGAACCTGAAAGAGAGAGATTACCTTTGTTGAAGAGAGCTGGGAAGTGGCCAGTTGGA 1320
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DB 1381 GCTCCATGTCAGAGATGAATTTCTTTCAGGAGGCCAGACTATGATGAACACTCAGCCAT 1440
QY 1441 CCCAAGCTGTTAAATTTCTATGAGTGTGTTTCAAGGAATACCCCATATACATAGTACT 1500
DB 1441 CCCAAGCTGTTAAATTTCTATGAGTGTGTTTCAAGGAATACCCCATATACATAGTACT 1500
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QY 1741 GTCGGAACAAAGTTCCTCAGTCAAGTGGTCCAGCTCCAGAGAGTGTTCATTTCAATATAC 1800
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DB 1801 AGCAGCAAGTCAGAGCTATGGCATTGGGATTCCTGATGTTGGAGAGTGTTCAGCCTGGGG 1860
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DB 1861 AAGCAGCCCTATGACTTGTATGACAACTCCCAAGTGGTGTCTGAAGTCTCCCAAGGCCAC 1920
QY 1921 AGGCTTTACCGGCCCCCTGSCATCGGACACCATCTACCAATCATGTACAGCTGCTGG 1980
DB 1921 AGGCTTTACCGGCCCCCTGSCATCGGACACCATCTACCAATCATGTACAGCTGCTGG 1980
QY 1981 CACGAGCTTCCAGAAAAGCGTCCCACTTTCCAGCACTCTGCTTCCATTTGAACCACTT 2040
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Db	2340	AAAGACTGAGCAGAACTGAAAAATTA	23999
Qy	2401	ATTGTGACACAAATTAATATATCTACCAAGTACAGAAATGTGAAA	2446
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RESULT 4			
AF045459			
LOCUS			
DEFINITION Homo sapiens Etk/Bmx cytosolic tyrosine kinase mRNA, complete cds.			
ACCESSION AF045459			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
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source			
CDS			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 2422; Conservative			
Qy			
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Qy			
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Qy			

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QY	1341	GAAGGGCAGTATGATGTGTGTTGAAGATGATCAAGGAGGCTCCATGTGAGAAGATGA	1400
DB	1492	GAAGGGCAGTATGATGTGTGTTGAAGATGATCAAGGAGGCTCCATGTGAGAAGATGA	1551
QY	1401	ATTCTTTCAGGAGCCAGACTATGATGAATCACTAGCCATCCCAAGCTGGTTAAATCTTA	1460
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DB	1672	CTTGCTGAATTAACCTGAGGAGTACGGAAGAGGACTTGAACCTTCCCAAGCTTTAGAAT	1731
QY	1581	GTGCTAGAGTCTGTGAGGATCGGCTTCTTGAGAGTACCAATTCATACACCGGGA	1640
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QY	1641	CTTGCTGCTGCTAACTGCTTGGTGGACAGAGATCTCTGTGGAAGTATCTGACTTTGG	1700
DB	1792	CTTGCTGCTGCTAACTGCTTGGTGGACAGAGATCTCTGTGGAAGTATCTGACTTTGG	1851
QY	1701	AATGACAAGGTATGTTCTTGATGACCAAGTATGTCAGTTCAGTCCGGAACAAAGTTTCCAGT	1760
DB	1852	AATGACAAGGTATGTTCTTGATGACCAAGTATGTCAGTTCAGTCCGGAACAAAGTTTCCAGT	1911
QY	1761	CAAGTGTGCTGAGTCCAGAGTGTTCATTTACTTCAAAATACAGCAGCAAGTCAGAGTATG	1820
DB	1912	CAAGTGTGCTGAGTCCAGAGTGTTCATTTACTTCAAAATACAGCAGCAAGTCAGAGTATG	1971
QY	1821	GGCATTGCGATCTGATGTGGAGGTGTTTCAGCTGCGGAGCAGCCCTATGACTTCTA	1880
DB	1972	GGCATTGCGATCTGATGTGGAGGTGTTTCAGCTGCGGAGCAGCCCTATGACTTCTA	2031
QY	1881	TGCAACTCCAGTGGTGTCTGAAGGTCTCCAGGGCCACAGGCTTTACCGGCCCCACCT	1940
DB	2032	TGCAACTCCAGTGGTGTCTGAAGGTCTCCAGGGCCACAGGCTTTACCGGCCCCACCT	2091
QY	1941	GGATCGGACACCATCTACAGATCATGTACAGCTGTGGCAGCAGCTTCCAGAAAAGCG	2000
DB	2092	GGATCGGACACCATCTACAGATCATGTACAGCTGTGGCAGCAGCTTCCAGAAAAGCG	2151
QY	2001	TCCACATTTTCAGCAACTCTGCTTCCATTTGAACCACTTCGGGAAAAGACAGCATTG	2060
DB	2152	TCCACATTTTCAGCAACTCTGCTTCCATTTGAACCACTTCGGGAAAAGACAGCATTG	2211
QY	2061	ARGAAGAAATAGGAGTGTGATAAGAAATGAATATAGATGTGGCCAGCATTTTCATTCA	2120
DB	2212	ARGAAGAAATAGGAGTGTGATAAGAAATGAATATAGATGTGGCCAGCATTTTCATTCA	2271
QY	2121	TTTTAAGAAATAGGAGGATTAAGTAATTTTAGTGTAGTTTAAATAGTGTCTCTGTA	2180
DB	2272	TTTTAAGAAATAGGAGGATTAAGTAATTTTAGTGTAGTTTAAATAGTGTCTCTGTA	2331
QY	2181	TTCTCTATTATTAGAAATCAACAGGACGGAACAAAGATTTCCCTTGAATTTAGATC	2240
DB	2332	TTCTCTATTATTAGAAATCAACAGGACGGAACAAAGATTTCCCTTGAATTTAGATC	2391
QY	2241	AAATAGTAAATTTGTTTATGCTGCTCCCTGATATAACACTTTCCAGCCCTATAGCAGAAG	2300
DB	2392	AAATAGTAAATTTGTTTATGCTGCTCCCTGATATAACACTTTCCAGCCCTATAGCAGAAG	2451
QY	2301	CACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTAAGACTTGAGCAGCACTGAA	2360
DB	2452	CACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTAAGACTTGAGCAGCACTGAA	2511

QY	2361	AAATTACTTATTGGATATTCAATCTTTCTTATATTGTCATCTGCACACAAATTAATA	2420
DB	2512	AAATTACTTATTGGATATTCAATCTTTCTTATATTGTCATCTGCACACAAATTAATA	2571
QY	2421	TACTACCAAGTACAGAAATGTGGAAAAAATAA 2453	
DB	2572	TACTACCAAGTACAGAAATGTGGAAAAAATAA 2604	
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DEFINITION	Sequence 3 from patent US 6326469.		
ACCESSION	ARI79663		
VERSION	ARI79663.1	GI:20221218	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2500)		
AUTHORS	Ullrich,A.; Gishizky,M. and Sures,I.		
TITLE	Megakaryocytic protein tyrosine kinases		
JOURNAL	Patent: US 6326469-A 3 04-DEC-2001;		
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BASE COUNT	819 a 505 c 553 g 623 t		
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Best Local Similarity	99.4%;	Pred. No. 0;	
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QY	22	ACGGATGATATATATGGATACAAAATCTATTCTAGAGAACTTCTTCTCAAAAGATCACAG	81
DB	70	AAGGATGATATATGGATACAAAATCTATTCTAGAGAACTTCTTCTCAAAAGATCACAG	129
QY	82	CAAAAGAGAAATGTCACCAAAATTAATTAAGAAGCGCTTTTGTGTTGACCAAAACA	141
DB	130	CAAAAGAGAAATGTCACCAAAATTAATTAAGAAGCGCTTTTGTGTTGACCAAAACA	189
QY	142	AACCTTCTCTACTATGAATATACAAAATGAAAAGGCGCAGAGAAAAGATCCATTGAA	201
DB	190	AACCTTCTCTACTATGAATATGACAAAATGAAAAGGCGCAGAGAAAAGATCCATTGAA	249
QY	202	ATTAAGAAATACAGATGTGTGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA	261
DB	250	ATTAAGAAATACAGATGTGTGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA	309
QY	262	CAGTACCCATTTCAGATGTCTATAAAGATGGGCTTCTCTATGTCTATGCATCAATGAA	321
DB	310	CAGTACCCATTTCAGATGTCTATAAAGATGGGCTTCTCTATGTCTATGCATCAATGAA	369
QY	322	GAGAGCCGAAGTCAGTGGTTGAAAGCATTACAAAAGAGATAAGGGTAACCCCACTG	381
DB	370	GAGAGCCGAAGTCAGTGGTTGAAAGCATTACAAAAGAGATAAGGGTAACCCCACTG	429
QY	382	CTGCTCAAGTACCATTAGTGGGTTCTTCTGTCGACGGGAAGTTCTCTGTGTGCCAGCAGC	441
DB	430	CTGCTCAAGTACCATTAGTGGGTTCTTCTGTCGACGGGAAGTTCTCTGTGTGCCAGCAGC	489
QY	442	TGTAAGCAGCCCGCAGGATGTACCCCTCTGCGGAGAGCATATGCTTAATCTGCACTGCA	501
DB	490	TGTAAGCAGCCCGCAGGATGTACCCCTCTGCGGAGAGCATATGCTTAATCTGCACTGCA	549
QY	502	AATGAAGAGAACACAGAGTTCCCACTTCCAGACAGAGTCTGAAAGTACCTCGGCA	561
DB	550	AATGAAGAGAACACAGAGTTCCCACTTCCAGACAGAGTCTGAAAGTACCTCGGCA	609
QY	562	GTTCTCTGTTTCAAAATGAGTGCACCTCTTCAAGTACCACTCTAGCCCAATATGACAA	621
DB	610	GTTCTCTGTTTCAAAATGAGTGCACCTCTTCAAGTACCACTCTAGCCCAATATGACAA	669

Best Local Similarity 99.4%; Pred. No. 0; Matches 2417; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY	22	ACGGATGATATATGATACAAATCTATTCTAGAGAACTCTCTCCAAAGATCAGAC	81
DB	70	AAGGATGATATATGATACAAATCTATTCTAGAGAACTCTCTCCAAAGATCAGAC	129
QY	82	CAAAAGAGAAATCTACCAATTAATACAAAGAACGGCTTTTGTGTTGACAAACA	141
DB	130	CAAAAGAGAAATCTACCAATTAATACAAAGAACGGCTTTTGTGTTGACAAACA	189
QY	142	AACCTTCTCTACTATGATATGACAAATGAAAGGGGAGAGAAAGATCCCAATGAA	201
DB	190	AACCTTCTCTACTATGATATGACAAATGAAAGGGGAGAGAAAGATCCCAATGAA	249
QY	202	ATTAAGAAATCAGATGTGGAGAAAGTAATCTCGAGGAGCAGACGCTGTAGAGAG	261
DB	250	ATTAAGAAATCAGATGTGGAGAAAGTAATCTCGAGGAGCAGACGCTGTAGAGAG	309
QY	262	CAGTACCCATTTTCAGATTGTCTATAAGATGGCTTCTATGCTATGCTATGCTATG	321
DB	310	CAGTACCCATTTTCAGATTGTCTATAAGATGGCTTCTATGCTATGCTATGCTATG	369
QY	322	GAGAGCCGAGTCACTGTGTTGAAAGCATTAACAAAGAGATAAGGGGTAAACCCACCTG	381
DB	370	GAGAGCCGAGTCACTGTGTTGAAAGCATTAACAAAGAGATAAGGGGTAAACCCACCTG	429
QY	382	CTGGTCAAGTACCATGATGGTCTTCTGAGCGGAAAGTTCCTGTGTTGCGAGAGC	441
DB	430	CTGGTCAAGTACCATGATGGTCTTCTGAGCGGAAAGTTCCTGTGTTGCGAGAGC	489
QY	442	TGTAAGCAGCCGAGGATGACCTCTGCGAGAGCATATGCTAACTGCATACTGCATC	501
DB	490	TGTAAGCAGCCGAGGATGACCTCTGCGAGAGCATATGCTAACTGCATACTGCATC	549
QY	502	AATGAAGAGAAACAGAGTTCACCTCTCCAGACAGAGTGTCTGAAGATACCTCGGCA	561
DB	550	AATGAAGAGAAACAGAGTTCACCTCTCCAGACAGAGTGTCTGAAGATACCTCGGCA	609
QY	562	GTTCTGTTCTCAAAATGGATGACCATCTTCAAGTACCATCTTACGCCAATATGACAAC	621
DB	610	GTTCTGTTCTCAAAATGGATGACCATCTTCAAGTACCATCTTACGCCAATATGACAAC	669
QY	622	CAATCAAGAGAAATCTATGGCTCCAGCCACCATCTTCAAGTACCATCTTACGCCAATAT	681
DB	670	CAATCAAGAGAAATCTATGGCTCCAGCCACCATCTTCAAGTACCATCTTACGCCAATAT	729
QY	682	GACAGCAACTCAAGAGAAATCTATGGCTCCAGCCACCATCTTCAAGTACCATCTTACCCA	741
DB	730	GACAGCAACTCAAGAGAAATCTATGGCTCCAGCCACCATCTTCAAGTACCATCTTACCCA	789
QY	742	AGGAGAGACTTCCCTGACTGTGGCAATGAGAAACTGAAAGTACGAGCAGCAGTAA	801
DB	790	AGGAGAGACTTCCCTGACTGTGGCAATGAGAAACTGAAAGTACGAGCAGCAGTAA	849
QY	802	GATGTTCAAGCAGTAAACAAAGAAAGAAATGTAATCACACCATCTCAAGATTTCA	861
DB	850	GATGTTCAAGCAGTAAACAAAGAAAGAAATGTAATCACACCATCTCAAGATTTCA	909
QY	862	TGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAAACCTTGGATGATTATCACTGG	921
DB	910	TGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAAACCTTGGATGATTATCACTGG	969
QY	922	TTTCTGTTAATCTCCAGATCAATCTGAACAGTTTACTCAGACAAAGGAAAGAA	981
DB	970	TTTCTGTTAATCTCCAGATCAATCTGAACAGTTTACTCAGACAAAGGAAAGAA	1029
QY	982	GGACATTTATGTTAGAAATTCAGCCCAAGTGGAAATGTCACAGTGTCTTATTTAGT	1041
DB	1030	GGACATTTATGTTAGAAATTCAGCCCAAGTGGAAATGTCACAGTGTCTTATTTAGT	1089
QY	1042	AAGSCTGTGATGATAAAGAGAACTCTCAAACTTACACAGTGCATACAAATGCTGAG	1101

DB	1090	AAGGCTGTGAATGATATAAAGAGAACTGTCAAAACATTTACACGTGCTACAAATGCTGAG	1149
QY	1102	AACAAATTTATACCTGGCAGAAAACTACTGTTTGTGATTTCCATTTCCAAAGCTTATTCAT	1161
DB	1150	AACAAATTTATACCTGGCAGAAAACTACTGTTTGTGATTTCCATTTCCAAAGCTTATTCAT	1209
QY	1162	CATCAACAATTCACGACGATGATCAGCGCTCGGCCACCTGTGTCAACAAAGGCC	1221
DB	1210	CATCAACAATTCACGACGATGATCAGCGCTCGGCCACCTGTGTCAACAAAGGCC	1269
QY	1222	AACAAGTCCCGACTCTGTGTCCTGGGAAATGGAATCTGGAACTGGAAGAGAGAG	1281
DB	1270	AACAAGTCCCGACTCTGTGTCCTGGGAAATGGAATCTGGAACTGGAAGAGAGAG	1329
QY	1282	ATTACCTTGTGAAGGAGCTGGGAAGTGCCAGTGTGGAGTGTGCTGAGCTGGCAAGTGG	1341
DB	1330	ATTACCTTGTGAAGGAGCTGGGAAGTGCCAGTGTGGAGTGTGCTGAGCTGGCAAGTGG	1389
QY	1342	AAGGGCAGTATGATGCTGTTAAGATCATCAAGGAGGCTCCATGTGTCAGAGATGAA	1401
DB	1390	AAGGGCAGTATGATGCTGTTAAGATCATCAAGGAGGCTCCATGTGTCAGAGATGAA	1449
QY	1402	TTCTTTTCAGAGGCCAGACTATGATGAACTCAGCCATCCCAAGCTGGTTAAATTTCTAT	1461
DB	1450	TTCTTTTCAGAGGCCAGACTATGATGAACTCAGCCATCCCAAGCTGGTTAAATTTCTAT	1509
QY	1462	GGAGTGTGTTCAAGGAATACCCCATATACATAGTACTGACTGAATATATAAGCAATGGCTGC	1521
DB	1510	GGAGTGTGTTCAAGGAATACCCCATATACATAGTACTGACTGAATATATAAGCAATGGCTGC	1569
QY	1522	TTGCTCAATACCTGAGGAGTACGCGAAAGAGCTTGAACCTTCCAGCTTCCAGAAATG	1581
DB	1570	TTGCTCAATACCTGAGGAGTACGCGAAAGAGCTTGAACCTTCCAGCTTCCAGAAATG	1629
QY	1582	TCCTAGAGTGTCTGTAAGGCTTTCCTTTCAGAGTCAACCAATTCATACACCGGAC	1641
DB	1630	TCCTAGAGTGTCTGTAAGGCTTTCCTTTCAGAGTCAACCAATTCATACACCGGAC	1689
QY	1642	TTGGTGTCTGTAAGTGTGTTGGACAGAGATCTCTGTGTGAAAGTATCTGACTTTTGA	1701
DB	1690	TTGGTGTCTGTAAGTGTGTTGGACAGAGATCTCTGTGTGAAAGTATCTGACTTTTGA	1749
QY	1702	ATGACAAGTATGTTCTTCTGATGACCATGATGTCAGTCCGACGAAAGTTCACAGTC	1761
DB	1750	ATGACAAGTATGTTCTTCTGATGACCATGATGTCAGTCCGACGAAAGTTCACAGTC	1809
QY	1762	AAGTGTGCTAGCTCCAGAGTGTTCATTTCAATACAGCAGCAAGTCAGAGTATGG	1821
DB	1810	AAGTGTGCTAGCTCCAGAGTGTTCATTTCAATACAGCAGCAAGTCAGAGTATGG	1869
QY	1822	GCATTTGGATCCTGATGTTGGAGTGTTCAGCTTGGGAGAGCAGCCCTATGACTTGTAT	1881
DB	1870	GCATTTGGATCCTGATGTTGGAGTGTTCAGCTTGGGAGAGCAGCCCTATGACTTGTAT	1929
QY	1882	GACAACCTCCAGGTGTTCTGAAAGTCTCCAGGGCCACAGGCTTTACCGGGCCCACTG	1941
DB	1930	GACAACCTCCAGGTGTTCTGAAAGTCTCCAGGGCCACAGGCTTTACCGGGCCCACTG	1989
QY	1942	GCATCGGACACCATCTACAGATCATGTACAGTGTGGCAGCAGCTTCCAGAAAGCGT	2001
DB	1990	GCATCGGACACCATCTACAGATCATGTACAGTGTGGCAGCAGCTTCCAGAAAGCGT	2049
QY	2002	CCACATTTACAGAACTCCTGCTTCCATTTGAACCTTTCGGGAAAGAAAGCAAGATTGA	2061
DB	2050	CCACATTTACAGAACTCCTGCTTCCATTTGAACCTTTCGGGAAAGAAAGCAAGATTGA	2109
QY	2062	AGAAGAAATTAGAGTGTGATAGAATGAAATATAGATGCTGGCCAGCATTTTCATTCAT	2121
DB	2110	AGAAGAAATTAGAGTGTGATAGAATGAAATATAGATGCTGGCCAGCATTTTCATTCAT	2169
QY	2122	TTTAGGAAGTAGAGGATTAAGTAAATTTTAGCTAGTTTTTAATAGTGTCTCTGTAT	2181
DB	2170	TTTAGGAAGTAGAGGATTAAGTAAATTTTAGCTAGTTTTTAATAGTGTCTCTGTAT	2229

Db	849	AGGGAAGACTCCCTGACTGGTGGCAAGTAAGAAAACGTAAAAAGTAGCAGCAGCAGTGAA	908
Qy	802	GATGTTGCAAGCAGTAACCAAAAAGAAAAGAAATGTGAATCACACCACCTCAAGATTTC	861
Db	909	GATGTTGCAAGCAGTAACCAAAAAGAAAAGAAATGTGAATCACACCACCTCAAGATTTC	968
Qy	862	TGGGAATTCCTGAGTCAAGTTCATCTCTGAAGAAGAGAAAACCTCGATGATTATGACTGG	921
Db	969	TGGGAATTCCTGAGTCAAGTTCATCTCTGAAGAAGAGAAAACCTCGATGATTATGACTGG	1028
Qy	922	TTTGCTGTACATCTCCAGATCACAATCTGAACAGTTTACTGACAGAAAAGGAAAGAA	981
Db	1029	TTTGCTGTACATCTCCAGATCACAATCTGAACAGTTTACTGACAGAAAAGGAAAGAA	1088
Qy	982	GGAGCATTTATGGTTAGAAATTCGAGCCCAAGTGGGAATGTACACAGTCTCCTATTAGT	1041
Db	1089	GGAGCATTTATGGTTAGAAATTCGAGCCCAAGTGGGAATGTACACAGTCTCCTATTAGT	1148
Qy	1042	AAGGCTGTGAATGATAAAAAAGGAACCTGCAAAATTTACCAGTGTCAATCAAAATGCTGAG	1101
Db	1149	AAGGCTGTGAATGATAAAAAAGGAACCTGCAAAATTTACCAGTGTCAATCAAAATGCTGAG	1208
Qy	1102	AACAAATTAACCTGGCGAGAAAACCTAGTGTGTTGATTCATCCATPCCAAAGCTTATTCATAT	1161
Db	1209	AACAAATTAACCTGGCGAGAAAACCTAGTGTGTTGATTCATCCATPCCAAAGCTTATTCATAT	1268
Qy	1162	CATCAACAAATTCAGCAGGCGATATCACAGGCTCCGCGCCACCTGTGTCAACAAGGCC	1221
Db	1269	CATCAACAAATTCAGCAGGCGATATCACAGGCTCCGCGCCACCTGTGTCAACAAGGCC	1328
Qy	1222	AACAAGTCCCGGACTCTGTCTCCTGGGAATGGAATCTGGGAATCAAAAAGAGAAG	1281
Db	1329	AACAAGTCCCGGACTCTGTCTCCTGGGAATGGAATCTGGGAATCAAAAAGAGAAG	1388
Qy	1282	ATTACCTTTGTAAGGAGCTGGGAAGTGGCCAGTTTGGAGTGGTCCAGCTGGCAGGTGG	1341
Db	1389	ATTACCTTTGTAAGGAGCTGGGAAGTGGCCAGTTTGGAGTGGTCCAGCTGGCAGGTGG	1448
Qy	1342	AAGGGCAGTATGATGTGCTGTTAAGATGATCAAGGAGGCTCCATGTCAGAGATGAA	1401
Db	1449	AAGGGCAGTATGATGTGCTGTTAAGATGATCAAGGAGGCTCCATGTCAGAGATGAA	1508
Qy	1402	TTCTTTTCAGGAGGCCAGACTATGATGAACCTCAGCCATCCAGCTGGTTAAATTCAT	1461
Db	1509	TTCTTTTCAGGAGGCCAGACTATGATGAACCTCAGCCATCCAGCTGGTTAAATTCAT	1568
Qy	1462	GGAGTGTGTTCAAAGGAATACCCCATATACATAGTACTGAATATATAGCAATGGCTGC	1521
Db	1569	GGAGTGTGTTCAAAGGAATACCCCATATACATAGTACTGAATATATAGCAATGGCTGC	1628
Qy	1522	TTGCTGAATTAACCTGAGAGTCAAGGAAAGGACTTGAACCTTCCAGCTCTTAGAAATG	1581
Db	1629	TTGCTGAATTAACCTGAGAGTCAAGGAAAGGACTTGAACCTTCCAGCTCTTAGAAATG	1688
Qy	1582	TGCTACCATGCTCTGAGGCGATCGCTCTTGGAGAGTCAACCAATTCATACACGGGAC	1641
Db	1689	TGCTACCATGCTCTGAGGCGATCGCTCTTGGAGAGTCAACCAATTCATACACGGGAC	1748
Qy	1642	TTGCTGCTGCTAACTGCTTGGTGGACAGAGATCTCTGTGTGAAGTATCTGACTTTGGA	1701
Db	1749	TTGCTGCTGCTAACTGCTTGGTGGACAGAGATCTCTGTGTGAAGTATCTGACTTTGGA	1808
Qy	1702	ATGCAAAAGGTATGTTCTTGATGACCAATATGCTAGTTTCAGTTCAGTTCGGAACCAAGTTCCAGTC	1761
Db	1809	ATGCAAAAGGTATGTTCTTGATGACCAATATGCTAGTTTCAGTTCAGTTCGGAACCAAGTTCCAGTC	1868
Qy	1762	AAGTGGTCAAGTCCAGAGGTGTTTCATTAATTAACAGAGAGTCAAGAGTATGAG	1821
Db	1869	AAGTGGTCAAGTCCAGAGGTGTTTCATTAATTAACAGAGAGTCAAGAGTATGAG	1928
Qy	1822	GCATTTGGGATCCGATGTGGAGGTGTTAGCCTTGGGAGCAGCCCTATGACTTGTAT	1881
Db	1929	GCATTTGGGATCCGATGTGGAGGTGTTAGCCTTGGGAGCAGCCCTATGACTTGTAT	1988
Qy	1882	GACAACTCCAGGTGGTCTTGAGGTCTCCAGGGCCACAGGCTTTACCGGCCCCACCTG	1941
Db	1989	GACAACTCCAGGTGGTCTTGAGGTCTCCAGGGCCACAGGCTTTACCGGCCCCACCTG	2048
Qy	1942	GCATCGGACACCATCTACAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAAGCGT	2001
Db	2049	GCATCGGACACCATCTACAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAAGCGT	2108
Qy	2002	CCACATTTTCAGCAACTCTCTGCTTCCATTTGAACCACTTCCGGGAAAAAGACAGCATGA	2061
Db	2109	CCACATTTTCAGCAACTCTCTGCTTCCATTTGAACCACTTCCGGGAAAAAGACAGCATGA	2168
Qy	2062	ACAAGAAATTAGAGTGTCTGATAAAGATGAATATAGATGCTGCCAGCATTTTCATTCAT	2121
Db	2169	ACAAGAAATTAGAGTGTCTGATAAAGATGAATATAGATGCTGCCAGCATTTTCATTCAT	2228
Qy	2122	TTTAAAGAAAGTAGGAAGGCATAGCTAAATTTAGCTAGTTTAAATAGTGTCTCTCTAT	2181
Db	2229	TTTAAAGAAAGTAGGAAGGCATAGCTAAATTTAGCTAGTTTAAATAGTGTCTCTCTAT	2288
Qy	2182	TGCTATTAATTTAGAAATGAACAGCAGGAACAAAGATTCCTTGAATTTAGATCA	2241
Db	2289	TGCTATTAATTTAGAAATGAACAGCAGGAACAAAGATTCCTTGAATTTAGATCA	2348
Qy	2242	AATTACTTAATTTGTTTATGCTGCTCCTGATATAACACTTTCCAGCCTATACAGAAC	2301
Db	2349	AATTACTTAATTTGTTTATGCTGCTCCTGATATAACACTTTCCAGCCTATACAGAAC	2407
Qy	2302	ACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTAAGACTGAGCAGAACTGAAA	2361
Db	2408	ACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTAAGACTGAGCAGAACTGAAA	2467
Qy	2362	AATTACTTAATTTGATTAATTCATTTCTTTTATATTGTCATTCACAAATTAATAT	2421
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE			
1 (bases 1 to 2609)			
AUTHORS			
Well, D., Power, M.A., Catterall, M. and Li, C.L.			
TITLE			
JOURNAL			
PUBLISHED			
REFERENCE			
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AUTHORS			
Well, D., Power, M.A., Catterall, M. and Li, C.L.			
TITLE			
JOURNAL			
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BASE COUNT	812 a 503 c 637 g 657 t
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Qy	7 ACGGAACAAGCTGAGCGGATGAATAATGGATACAAATCTATTCTAGAGAACTTCTT 66
Db	115 ACAGAGGAGGCCAAATGGAGCAGACATATGAGAGTAATAATCAATCTCGAGAGAACTGCTT 174
Qy	67 CTCAAAAGATCACAGCAAAAGAGAAATGTCAACCAATAATATCAAAAGACGGCTTTT 126
Db	175 CTCAAAAGTCACAGCAAAAGAGAAATGTCAACCAATAATATCAAAAGACGGCTTTT 234
Qy	127 GTTTTGACCAAAACAACTTTCTCTACTATGATGACAAATGACAAATGACAAAGGGGACGAGA 186
Db	235 GTTCCTACCAAAACAACTTTCTCTACTATGATGACAAATGACAAATGACAAAGGGGACGAGA 294
Qy	187 AAAGGATCCATTGAAATTAAGAAATCAGATGTGTGGAGAAATGAAATCTCGAGAGAGCAG 246
Db	295 AAAGGATCAATAGAAATTAAGAAATCAGATGTGTGGAGAAATGAAATCTCGAGAGAGCAG 354
Qy	247 ACGCCTGTAGAGACAGTACCCATTCAGATGTCTATAAAGATGGCTTCTCTATGTC 306
Db	355 ACACGGTGGAGACAGTACCCATTCAGATGTGTATAAAGATGGCTTCTCTATGTC 414
Qy	307 TATGCATCAATGAAGAGACCGGAGTCAGTGGTGAAGCATTTACAAAGAGATAGG 366
Db	415 TATGCATCGAATGAAGAGACCGGATGTCAGTGGTTAAAGCGCTGCAAAAGAGATAGCG 474
Qy	367 GGTAACCCCACTGCTGGTCAAGTACCATGAGTGGTTCCTCGTGACGGGAAGTTCCTG 426
Db	475 GGCAACCCCTCACTGTTGATCAAGATATCAGATGGCTTCTTGTGATGGAAGTTCCTG 534
Qy	427 TGTTGCCAGCAGAGCTGTAAAGCAGCCCGCAGGATGTACCCCTCTGGGAAGCATATGCTAAT 486
Db	535 TGTTGCCAGCAGAGCTGTAAAGCAGCCCGCAGGATGTACCTCTCTGGAGAGCATATGCTGAT 594
Qy	487 CTGCATCTCAGTCAATGAGAGAAACACAGAGTTCCTCCACTTCCAGACAGAGTGGTG 546
Db	595 CTGCATCTCAGTCAATGAGAGAAACACAGAGTTCCTCCACTTCCAGAGAGAGCTACTG 654
Qy	547 AAGTACCTCGGGCAGTTCCTGTTCTCAAAATGGATGACCAATCTTCAAGTACCACCTCTA 606
Db	655 AAGATTCCAAGGCGAGTTCCTGTTCTCAAAATGGATGATCATCTTCAGGTGCCATCTCA 714
Qy	607 GCCCAATATGACAGCAATCAAGAAACATATGGCTCCAGCCACCACTTTCAGATACC 666
Db	715 CCC----- 717
Qy	667 AGCTAGCGCAATATGACAGCAACTCAAGAAATCTATGGCTCCAGCCAACTTCAAC 726
Db	718 -----CAATATGACAGTATTTCAAGAAAGTTGTGTTCCTCCAGCCAACTTCAAC 768
Qy	727 ATGAGTATATTCAGGGAGAGACTTCCCTGACTGTGTGGCAAGTAAGAAACTGAGAAAGT 786
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Db	826	-----AGCGAGGAGACATTGCATGCAGTAACCAACTGAAAGAAATATCGCCTCTCAC	879
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Db	880	AGCAGCTCAAGAGATTCATGGGATTCCTCGAGTCAAGTTCATCAAGAAAGAGGAAAT	939
Qy	904	CTGGATGATTTATGACTGGTTTCTGTAACATCTCCAGATCAAACTCTGAACAGTACTC	963
Db	940	CTGCATGCTTATGACTGGTTCTCGGGAATATCTCCAGGTCAAACTCTGAGCAGTACTG	999
Qy	964	ACACAAAAGGGAAGAGAGCAATTTATGTTTGAATAATTCGAGCCAACTGGGAATGTAC	1023
Db	1000	AGACAAAAGGGAAGAGAGCAATTTATGTTTGGAAATTCAGCCAGATGGGAATGTAC	1059
Qy	1024	ACAGTGTCTTATTTAGTAGAGGCTGTGAATGATAAAAAAGGACTCTCAACATACCAC	1083
Db	1060	ACTGTGTCTTATTTAGTAGAGGCTGTGAATGATAAAAAAGGACTCTCAACATACCAC	1119
Qy	1084	GTGCATACAAATCTCGAGAACAAATATATACCTGGCAGAAACACTACTCTTTGATTCCATT	1143
Db	1120	GTGCATACTATGCTGAAATTAATATATACCTGGCTGAAACACTACTCTTTGATTCCATT	1179
Qy	1144	CCAAAGCTTATTCATTCATCAACAAATTCAGCAGGATGATCACGGCTCCGCCAC	1203
Db	1180	CCAAAGCTTATTCATTCATCAACAAATTCAGCAGGATGATCACGGCTCCGCCAC	1239
Qy	1204	CCTGTGTCAACAAAGGCCAACAAAGTCCCGACTCTGTCTCCCTGGGAATGGAATCTGG	1263
Db	1240	CCAGTGTCAACAAAGGCCAACAAAGTCCCGGTCTGTCTGGCTGGGAAGTGAATTTGG	1299
Qy	1264	GAACCTGAAAGAGAGAGATTAACCTTGTGTAAGAGCTGGGAGTGGCCAGTTTGGAGTG	1323
Db	1300	GAACCTGAAAGAGAGAGATTAACCTTGTGTAAGAGCTGGGCAATGGCCAGTTTGGAGTG	1359
Qy	1324	GTCCAGCTGGGCAAGTGGAGGGGAGTATGATGTTGCTGTGTAAGATGATCAAGAGGGC	1383
Db	1360	GTCCAGCTGGGCAAGTGGAGGGGAGTATGATGTTGCTGTGTAAGATGATCAAGAGGGT	1419
Qy	1384	TCCATGTCAAGAGATGAATTTCTTCAGGAGGCCAGACTATGATGAACCTCAGCCATCCC	1443
Db	1420	GCCATGTCAAGAGATGAATTTCTTCAGGAGGCCAGACTATGATGAACCTCAGCCATCCC	1479
Qy	1444	AAGCTGGTTAAATTTCTATGAGTGTGTTCAAGAGAAATACCCCATATACATAGTACTGAA	1503
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Qy	1504	TATATAAGCAATGGCTGCTGCTGAATTAACCTGAGGAGTACCGGAAAGAGACTTGAACCT	1563
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Qy	1564	TCCAGCTCTTGAAGATGCTACGATGCTGTGAAGGATGGCTTCTTGGAGAGTCAAC	1623
Db	1600	TCCAGCTCTTGAAGATGCTATGATGCTGTGAAGGATGGCTTCTTGGAGAGCCAT	1659
Qy	1624	CAATTCATACACCGGAGCTTGGCTGCTGCTAACTGCTGTGGGACAGAGATCTCTGTGTG	1683
Db	1660	CAGTTTCATACATCGAGATTTGGCTGCTCGGAACTGTTGGTGACAGATGATCTCTGTG	1719
Qy	1684	AAAGTATCTGACTTTGGAAATGACAGGATGTTCTTGTGATGACCACTATGTCAGTTCACTC	1743
Db	1720	AAAGTATCTGACTTTGGAAATGACAGGATGTTCTTGTGATGACCACTATGTCAGTTCACTC	1779
Qy	1744	GGAACAAAGTTTCCAGTCAAGTGGTTCAGCTCCAGAGGTGTTTCTTACTTCAATACAGC	1803
Db	1780	GGAACAAAGTTTCCAGTCAAGTGGTTCAGCTCCAGAGGTGTTTCTTACTTCAATACAGC	1839
Qy	1804	AGCAAGTCAGAGCTATGGCATTGGGATTCCTGATGTGGGAGGTGTTTCACTCTAGGGAAG	1863
Db	1840	AGCAAGTCAGAGCTATGGCATTGGGATTCCTGATGTGGGAGGTGTTTCTAGTCTAGGGAAG	1899
Qy	1864	CAGCCCTATGACTTGTATGACAACTCCCAAGGTGTTCTGAAGTCTCCCAAGGCCACAGG	1923

Db	1900	CAGCCCTATGACTTATATGATTAACCGAGGTGGTGTGAGGTCTCCAGGGCCACACA	1959
QY	1924	CTTTACCGGCCCCACCTGGCATCGGACACCATCTACAGATCATGTACAGCTGCTGGCAC	1983
Db	1960	CTCTACCGGCCCCCACTGGCATCGACACCATCTACAGATCATGTACAGCTGCTGGCAT	2019
QY	1984	GAGCTTCCAGAAAGCGTCCACATTTCCAGCAACTCCCTGCTCTCCATTAAGCAACCTCGG	2043
Db	2020	GAGCTTCCAGAAAGCGGCCCACTTCCAGCAACTCCCTGCTCTCCATTAAGCAACCTCGG	2079
QY	2044	GAAGAAAGCAAGCATTTAGAGAAAGAAATAGGAGTCTGATAGAAATGAATATAGATGCTG	2103
Db	2080	GAACAAGATAAACCATGAAGAGAAATTTTCAGAGTGGTGTATGAGAAACAATGCAATATTA	2139
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Db	2140	ACTAACACATCTCATTTGTTGAAGGAAGTAGAAGAGCACTCAATGCAATGTACTGCTCT	2199
QY	2164	TAATAGTGTCTCTGATTTGCTATTTATTTA-----GAAATGAACAAGCAGCA	2212
Db	2200	TAACATGCTGTATGCTGTCTATCTGTATATATCTACCAAAAAAGCAAGGTAGGA	2259
QY	2213	AACAAAGATTCCTTGAATTTAGATCAAAATAGTAATTTTGTATGCTGCTCCTGA	2272
Db	2260	AACAAGATAGTCTTTGAATTTAGTCAAAATGCTAATTTG-TTTGCTGCTTTTAA	2318
QY	2273	TATACACTTTCAGCCCTTAGCAGAACACATTTTCAGACTGCAATATAGAGACTGTGT	2332
Db	2319	GGT-ATACTTCAAGACTATGTTAGAGTTCATTTTATAGATGCAATTTACAAATGTATC	2377
QY	2333	TCATGTGAAGAGCTGACGACACTGAAATATCTATTGATATTCATCTTTCT--	2390
Db	2378	T-GGTATGAAGTAGACGAATTTGAAAGGTGATTTGTTGGGAAGTCTTTTAA	2436
QY	2391	--TTATATGTCTGTCACACAAATTAATATCTACCAAGTACAGAAATGT	2441
Db	2437	AAAAAATGGCACTAGTGTGATTAATTAATATCTTTTCAGAACGGAATGT	2489
RESULT 9			
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LOCUS	AF012104	2369 bp mRNA linear	ROD 09-OCT-1997
DEFINITION	Mus musculus cytoplasmic tyrosine kinase (bmX) mRNA, complete cds.		
ACCESSION	AF012104		
VERSION	AF012104.1	GI:2293557	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 2369)		
AUTHORS	Ekman,N., Lymboussaki,A., Vastrik,I., Sarvas,K., Kaipainen,A. and Alitalo,K.		
TITLE	Bmx tyrosine kinase is specifically expressed in the endocardium and the endothelium of large arteries		
JOURNAL	Circulation 96 (6), 1729-1732 (1997)		
MEDLINE	97462826		
PUBMED	9323053		
REFERENCE	2 (bases 1 to 2369)		
AUTHORS	Ekman,N. and Alitalo,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-JUL-1997) Molecular/Cancer Biology Laboratory, Haartman Institute, P.O.B 21 (Haartmaninkatu 3), Helsinki 00014, Finland		
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QY	806	TTGCAAGCAGTAACCAAAAGAAAGAAAT---GTGAATACACACACCTCAAGAGATTTCAT	862
Db	706	TTGCAATGAGTAACTGAAAGAAATATCGCCTCTCAGCAGCAGTCAAGAGATGTCAT	765
QY	863	GGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAAACCTCGATGATATGACGTGT	922
Db	766	GGGATTCCTGAGTCAAGTTCATCAGAAGAGAGGAAATCTGCATGCTTATGACTGGT	825
QY	923	TTGCTGTTAACTCCAGATCACAATCTGACAGTGTACTCAGACAAAGGAAAGAG	982
Db	826	TTGCTGGGAATATCTCAGGTGCAATCTGAGCAGTGTACTGAGACAAAGGAAAGAG	885
QY	983	GAGCATTTATGTTAGAAATTCGAGCCAAAGTGGGAATGTACACAGTGTCTTATTTAGTA	1042
Db	886	GAGCATTTATGTTGCGGAATTCAGCCAGATGGGAATGTACACAGTGTCTTATTTAGTA	945
QY	1043	AGGCTGTGAATGATAAAAAGGAAGTGTCAACATATTACCAGTGCATACAAATGCTGAGA	1102
Db	946	AGGCTGTGAATGATAAAAAGGAAGTGTCAACATATTACCAGTGCATACAAATGCTGAGA	1005
QY	1103	ACAAATTTATCTGCGCAAAACTACTGTTTGTGATTCATTCCAAAGCTTATTCATTATC	1162
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QY	1163	ATCAACAAATTCAGCAGCATGATCACACGGCTCGGCCACCCCTGTGTCAACAAAGGCCA	1222
Db	1066	ACCAACATAATTCAGCAGCATGATCACACGGCTCGGCCACCCAGTGTCAACCAAGGCCA	1125
QY	1223	ACAGGTCCCGGACTCTGTGCCCTGGGAATGGAATCTGGGAAGTGTGGAAGTGTGGAAGAGA	1282
Db	1126	ACAAAGTCCCGGCTGTGTGCCCTGGGAAGTGTGGAAGTGTGGAAGTGTGGAAGAGA	1185
QY	1283	TTACTTGTGTAAGGAGTGGGAAGTGGCCAGTTGGAGTGGTCCAGCTGGGCAAGTGA	1342
Db	1186	TTACTTGTGTAAGGAGTGGGCAATGGCCAGTTGGAGTGGTCCAGCTGGGCAAGTGA	1245
QY	1343	AGGGCAGTATGATGTTGCTGTTAAGATGATCAAGAGGGCTCCATGTCAGAGATGAAT	1402
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QY	1403	TCCTTCAGGAGGCCAGACTATGATGAAACTCAGCCATCCCAAGCTGGTAAATCTATG	1462
Db	1306	TCCTTCAGGAGGCCAGACTATGATGAAACTCAGCCATCCCAAGCTGGTAAATCTATG	1365
QY	1463	GAGTGTGTTCAAGGAATACCCCATATACATAGTACTGAATATATAGCAATGCTGCT	1522
Db	1366	GAGTGTGTTCAAGGAATACCCCATCTATATAGTAACTGAGTATATACAAATGCTGCT	1425
QY	1523	TGCTGAATTTACCTGAGGAGTCAAGGAAGGACTTGAACCTTCCAGCTCTTAGAAATGT	1582
Db	1426	TGCTGAATTTACCTGAGGAGTCAAGGAAGGACTTGAAGTGTGCAAGCTCTTAGAAATGT	1485
QY	1583	GCTACGATGCTGTGAAGGCAATGCCCTTCTTGGAGAGTCAACCAATTCATACACCGGACT	1642
Db	1486	GTTATGATGCTGTGAAGGCAATGCCCTTCTTGGAGAGCCATCAGTTCATACATCGAGATT	1545
QY	1643	TGGCTGCTGTAACCTGCTGTGTGACAGAGATCTCTGTGTGAAAGTATCTGACCTTGA	1702
Db	1546	TGGCTGCTGGAAGTGTGTGTGTGACAGTGTCTCTGTGAAAGTCTCAGAGCTTGA	1605
QY	1703	TGACAAGTATGTTCTGATCAGCAGTATGTCAGTTCAGTCCGAGCAAGTTCACATCA	1762
Db	1606	TGACGAGATATGCTCTGATGATCAGTATGTCAGTTCAGTCCGAGCAAGTTCACATCA	1665
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Db	1666	AGTGGTCAGCTCCAGAGTGTGTTTCTTACTTCAATACAGCAGCAAGTTCAGCTATGGG	1725
QY	1823	CATTTGGATCCTGATGTTGGAGGTGTTACGCTCGGGAAGCAGCCCTATGACTGTATG	1882
Db	1726	CATTTGGATCCTGATGTTGGAGGTGTTAGTCTAGGGAAGCAGCCCTATGACTGTATG	1785
QY	1883	ACAATCCACAGTGTCTTGAAGGTCTCCAGGGCCACAGGCTTTACCGGCCACCTGG	1942
Db	1786	ATAACTCCAGGTGTTGTGAAGGTCTCCAGGGCCACAGACTCTACCGGCCACCTGG	1845
QY	1943	CATCGGACACCATCTACAGATCATGTACAGTGTGCGCAGCAGCTTCAGAAAAAGCGTC	2002
Db	1846	CATCAGACACCATCTACAGATCATGTACAGTGTGCGCAGCAGCTTCAGAAAAAGCGTC	1905
QY	2003	CCACATTCACCAACTCCTGCTTCCATTGAACCACTTCGGGAAAAAGCAAGCATTTGAA	2062
Db	1906	CCACATTCACCAACTCCTGCTGCGCATGAACCACTTCGGGAAAAAGCAAGCATTTGAA	1965
QY	2063	GAAGAAATTTAGAGTGTGATAAGAAATGAATATAGTGTGCGCAGCAGCTTTTCATTTAT	2122
Db	1966	GAGAAATTCAGAGTGTGATAAGAAATGAATATAGTGTGCGCAGCAGCTTTTCATTTAT	2025
QY	2123	TTAAGGAAGTAGGAAGCATAAAGTAATTTAGCTAGTGTGTTTAAATAGTGTCTCTGATTT	2182
Db	2026	GTAGGGAAGTAGGAAGCACTTAAAGCAATGTAGCTGCTTCTTAAACAATGGTCTATGGCT	2085
QY	2183	GTCTATTATTATA-----GAAATGAACAGGAGGAGGAAACAAAGATTCCCTTGAA	2231
Db	2086	GTCTATTATTATACTACCAAAAAAGCAAGTAGGAAACAAAGATGTTCTTTGAA	2145
QY	2232	ATTTAGATCAAAATAGTAATTTTGTGTTATGCTGCTCCTGATATACACTTTCCAGCCCTA	2291
Db	2146	ATTTAGGTCAAATGGTAATTTTG-TTGTGCTGCTTTTAAAGGT-ATACTTCCAAGACTA	2203
QY	2292	TAGCAGAGCAGCATTTTCAGACTGCAATATAGAGACTGTGTCATGTGTAAGACTGAGC	2351
Db	2204	TGGTAGAAGTTCATTTTAGATTGCAATTTACAAATTTGACT-TGTATTAAGGTAGAGC	2262
QY	2352	AGAACTGAAAAATTAATTTAGTATGGAATTCATTTCTTTCT-----TTATATTGCTATGTC	2407
Db	2263	AGAAATGGAAGGTGATTTGTTGGAACTCCCTTTTTTAAAAAAAATTTGGCACTAGTG	2322
QY	2408	CAACAATTAATATATACCTACCAAGTACAGAAATGTGGAAGAAAAA 2453	
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LOCUS	AX718901	2468 bp	DNA linear PAT 15-APR-2003
DEFINITION	Sequence 3 from Patent WO0238797.		
ACCESSION	AX718901		
VERSION	AX718901.1 GI:29891466		
KEYWORDS	Mus sp.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Mcatee,P.		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
JOURNAL	Modulators of bruton's tyrosine kinase, their identification and use		
FEATURES	Patent: WO 0238797-A 3 16-MAY-2002;		
source	Bristol-Myers Squibb Company (US)		
BASE COUNT	713 a 559 c 602 g 594 t		
ORIGIN	1..2468		
Query Match	20.1%; Score 494.6; DB 6;		
Best Local Similarity	64.0%; Pred. No. 1.2e-110;		
Matches 746; Conservative	0; Mismatches 419; Indels 0; Gaps 0;		


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ORIGIN

Query Match 20.1%; Score 494.6; DB 10; Length 2493;
Best Local Similarity 64.0%; Pred. No. 1.2e-110;
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QY 905 CTGAAGCTGAGGACTCCATGAGATGATGAGTGATTTCCAAAGCAGATGCTCGAAGTC 964
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 947 AATCTGAACAGTTACTCAGACAAAAGGAAAGAGGAGCATTTATGGTTAGAAAATCGA 1006
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 965 AAGCTGAGCACTGCTAAGCAAGAGGAGGAGAGGAGGTTTCATTTGTCGAGACTCCA 1024
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1007 GCCAAGTGGGAATGACAGAGTGCTCTTATTTAGTAGGCTGTGAATGATAAAAAGGAA 1066
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1067 CTGTCAAAACATTACCACGTGCATACAAATGCTGAGAACAAATATACCTGGCAGAAACT 1126
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QY 1085 TGATCCGGCATTACCTGTGTGTTCCAGCCACAGAGCCAGTATTACCTGGCTGAGAAAC 1144
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QY 1127 ACTGTTTGTGATTCATTCCTCAAGCTTATTCATTCATCAACAAATTCAGCAGGACATGA 1186
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QY 1145 ACCCTTCAGCACCATCTCTGAGCTCATTAATCACTACCAACAACTCTGAGGCCTCA 1204
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QY 1187 TCACACGCTCGGCCACCTGTGTCAACAAAGGCCAACAAAGTCCCGACTCTGTGTCC 1246
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QY 1865 TCTACTCCCTGGGAGAGTCCGTATGAGAGATTACTACAGTGGAGGACAGACACA 1924
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QY 1907 TCTCCAGGCGCACAGGCTTTACCGGCCACCTCGCATCGGACACCATCTACAGATCA 1966
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QY 1925 TTGCTCAAGGCTTACGCTCTACAGGCTCATCTGGCATCAGAGAGGATATACCATCA 1984
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QY 1985 TGTACAGCTGCTGGCAGGAGAAAGCAGATGACGCTCTAGTTTCAAAATTTCTCTTGAGTA 2044
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RESULT 13
MUSBPB 2485 bp mRNA linear ROD 27-APR-1993
LOCUS Mus musculus B cell cytoplasmic tyrosine kinase (BPK) mRNA, complete cds.
ACCESSION L08967
VERSION L08967.1 GI:192233
KEYWORDS tyrosine kinase.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2485)
AUTHORS Tsukada, S., Saffran, D.C., Rawlings, D.J., Parolini, O., Allen, R.C., Klisak, I.J., Kubagawa, H., Mohandas, T.K., Quan, S., Belmont, J.W., Cooper, M.D., Conley, M.E. and Witte, O.N.
TITLE Deficient expression of a B cell cytoplasmic tyrosine kinase in human X-linked agammaglobulinemia
JOURNAL Cell 72 (2), 279-290 (1993)
MEDLINE 93145329
PUBMED 8425221
COMMENT Original source text: Mus musculus (strain C57BL/6 x DBA/2) pre-B cell cDNA to mRNA.
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ACCESSION I25434
VERSION I25434.1 GI:1605304
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2505)
AUTHORS Witte,O., Tsukada,S., Saffran,D. and Rawlings,D.
TITLE Hematopoietic restricted tyrosine kinase (BPK)
JOURNAL Patent: US 5550054-A 1 27-AUG-1996;
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GenCore version 5.1.6
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Listing first 45 summaries

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ALIGNMENTS

RESULT 1

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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1476:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2456 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g951234
; US-09-016-434-1476

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1201	CACCTGTGTCAACAAAGGCCAACAAAGTCCCGACTCTGTCTCCCTGGGAATGGAATC	1260
Db	1201	CACCTGTGTCAACAAAGGCCAACAAAGTCCCGACTCTGTCTCCCTGGGAATGGAATC	1260
QY	1261	TGGAACTGAAAGAGAGATTAACCTTGTGTAAGAGAGCTGGGAAGTGGCCAGTTTGA	1320
Db	1261	TGGAACTGAAAGAGAGATTAACCTTGTGTAAGAGAGCTGGGAAGTGGCCAGTTTGA	1320
QY	1321	GTGCTCCAGCTGGGCAAGTGAAGGGCAGTATGATGTTGCTGTTAAAGATGATCAAGAG	1380
Db	1321	GTGCTCCAGCTGGGCAAGTGAAGGGCAGTATGATGTTGCTGTTAAAGATGATCAAGAG	1380
QY	1381	GGCTCCATGTCAGAAAGATGAATTCCTTTCAGGAGGCCAGACTATGATGAACCTCAGCCAT	1440
Db	1381	GGCTCCATGTCAGAAAGATGAATTCCTTTCAGGAGGCCAGACTATGATGAACCTCAGCCAT	1440
QY	1441	CCCAAGCTGGTAAATTCATATGGAGTGTGTTCAAAAGGAATACCCCATATACATAGTACT	1500
Db	1441	CCCAAGCTGGTAAATTCATATGGAGTGTGTTCAAAAGGAATACCCCATATACATAGTACT	1500
QY	1501	GAATATATAAGCAATGCTGCTGAATTAACCTGAGGAGTACGGAAGAGACTGTAA	1560
Db	1501	GAATATATAAGCAATGCTGCTGAATTAACCTGAGGAGTACGGAAGAGACTGTAA	1560
QY	1561	CTTCCCAGCTTTAGAAATGTGCTACGATCTCTGAGGAGTGCCTTCTTGGAGAGT	1620
Db	1561	CTTCCCAGCTTTAGAAATGTGCTACGATCTCTGAGGAGTGCCTTCTTGGAGAGT	1620
QY	1621	CACCAATTCATACACCGGAGTGTGCTGCTGTAACCTGCTGAGGAGTGCCTTCTG	1680
Db	1621	CACCAATTCATACACCGGAGTGTGCTGCTGTAACCTGCTGAGGAGTGCCTTCTG	1680
QY	1681	GTGAAAGTATCTGACTTTTGGAAATGACAAAGTATGTTGATGACAGTATGTCAGTTCA	1740
Db	1681	GTGAAAGTATCTGACTTTTGGAAATGACAAAGTATGTTGATGACAGTATGTCAGTTCA	1740
QY	1741	GTGGAACAAAGTTTCCAGTCAAGTGTGCTGAGGAGTGTGTTCAATCTCAAAATAC	1800
Db	1741	GTGGAACAAAGTTTCCAGTCAAGTGTGCTGAGGAGTGTGTTCAATCTCAAAATAC	1800
QY	1801	AGCAGCAAGTCAGAGTATGGGATTCCTGATGTTGGAGTGTGTTCAAGCTGGGG	1860
Db	1801	AGCAGCAAGTCAGAGTATGGGATTCCTGATGTTGGAGTGTGTTCAAGCTGGGG	1860
QY	1861	AAGCAGCCCTATGACTTGTATGACAACTCCAGGTTGTTCTCAAGGTTCCAGGGCCAC	1920
Db	1861	AAGCAGCCCTATGACTTGTATGACAACTCCAGGTTGTTCTCAAGGTTCCAGGGCCAC	1920
QY	1921	AGGCTTTTACCGGCCCCCTGCGATCGGACACCATCTACCATCATGTTACAGTCTCGG	1980
Db	1921	AGGCTTTTACCGGCCCCCTGCGATCGGACACCATCTACCATCATGTTACAGTCTCGG	1980
QY	1981	CACGAGCTTCCAGAAAAGCGCCCACTTTTCAGCAACTCCTCTCTTCCATTGAACACATT	2040
Db	1981	CACGAGCTTCCAGAAAAGCGCCCACTTTTCAGCAACTCCTCTCTTCCATTGAACACATT	2040
QY	2041	CGGAAAAGAACAGCATTTGAAGAAATTAGGAGTGTGATAGAAATGAATATAGATG	2100
Db	2041	CGGAAAAGAACAGCATTTGAAGAAATTAGGAGTGTGATAGAAATGAATATAGATG	2100
QY	2101	CTGGCCAGCATTTTCATTTCAATTTTAAAGAAAGTAGGAGGCATAGTAATTTAGTAGT	2160
Db	2101	CTGGCCAGCATTTTCATTTCAATTTTAAAGAAAGTAGGAGGCATAGTAATTTAGTAGT	2160

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Db 2349 ACATTTTCAGACTCAATATATAGACACTGTGTTTCATGTGTAAGACTGAGCAGAACTGAAA 2408
QY 2362 AATTACTATTGGATATTCATCTTTCTTTATATTTGTCATTTGTCACAACTTAAATAT 2421
Db 2409 AATTACTATTGGATATTCATCTTTCTTTATATTTGTCATTTGTCACAACTTAAATAT 2468
QY 2422 ACTACCAAGTACAGAAATGTGGAAAAA 2453
Db 2469 ACTACCAAGTACAAAAA 2500

RESULT 4
PCT-US95-05008-3
; Sequence 3, Application PC/TUS9505008
; GENERAL INFORMATION:
; APPLICANT: Sugen, Inc.
; APPLICANT: 515 Galveston Drive
; APPLICANT: Redwood City, California 94063-4720
; APPLICANT: United States of America
; APPLICANT: Wissenschaften E.V.
; APPLICANT: Hofgarten Str. 2
; APPLICANT: Munchen 80539
; APPLICANT: Germany
; TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05008
; FILING DATE: 24-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
PCT-US95-05008-3

Query Match 97.6%; Score 2397.6; DB 5; Length 2500;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2417; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 22 ACGGATGATATATGATGATACAAATCTATTCTAGAAAGTCTTCTCAAAAGATCACAG 81
Db 70 AAGSATGATATATGATGATACAAATCTATTCTAGAAAGTCTTCTCAAAAGATCACAG 129
QY 82 CAAAAGAGAAATGTCACCAAAATATACAAAGAACGGCTTTTGTGTTGACCAAAACA 141

Db 130 CAAAAGAGAAATGTCACCAAAATATACAAAGAACGGCTTTTGTGTTGACCAAAACA 189
QY 142 AACCTTTCCCTACTATGATATGACAAATATGAAAGGGGCAGCAGAAAAGGATCCATTGAA 201
Db 190 AACCTTTCCCTACTATGATATGACAAATATGAAAGGGGCAGCAGAAAAGGATCCATTGAA 249
QY 202 ATTAAGAAAATCAGATGTGTGGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA 261
Db 250 ATTAAGAAAATCAGATGTGTGGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA 309
QY 262 CAGTACCCATTTCAGATTTCTATATAAGATGGGCTTCTCTATGTCTATGTCATCAATGAA 321
Db 310 CAGTACCCATTTCAGATTTCTATATAAGATGGGCTTCTCTATGTCTATGTCATCAATGAA 369
QY 322 GAGAGCCGAAGTCAGTGGTTGAAAGCATTAACAAAAGAGATAAGGGGTAAACCCACCTG 381
Db 370 GAGAGCCGAAGTCAGTGGTTGAAAGCATTAACAAAAGAGATAAGGGGTAAACCCACCTG 429
QY 382 CTGCTCAAGTACCATTAGTGGTTCTTCTGTCGACGGGAAGTTCTCTGTGTGTCAGAGAGC 441
Db 430 CTGCTCAAGTACCATTAGTGGTTCTTCTGTCGACGGGAAGTTCTCTGTGTGTCAGAGAGC 489
QY 442 TGTAAAGCAGCCCGAGGATGTACCTCTGCGGAAGCATATGCTAAATCTGCATACTCGAGTC 501
Db 490 TGTAAAGCAGCCCGAGGATGTACCTCTGCGGAAGCATATGCTAAATCTGCATACTCGAGTC 549
QY 502 AATGAAGAGAAACACAGAGTTCCACCTTCCAGACAGAGTGTGGAAGATACCTCGGGCA 561
Db 550 AATGAAGAGAAACACAGAGTTCCACCTTCCAGACAGAGTGTGGAAGATACCTCGGGCA 609
QY 562 GTTCTCTGTTCTCAAAATGGATGCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 621
Db 610 GTTCTCTGTTCTCAAAATGGATGCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 669
QY 622 GAATCAAGAAAATCTATGGCTCCAGCCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 681
Db 670 GAATCAAGAAAATCTATGGCTCCAGCCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 729
QY 682 GACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 741
Db 730 GACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCATCTTCAAGTACCACCATCTTCAAGTACCACCAT 789
QY 742 AGGGAAGACTTCCCTGACTGTGGCAAGTAGAAAACCTGAAAAGTAGCAGCAGCTGAA 801
Db 790 AGGGAAGACTTCCCTGACTGTGGCAAGTAGAAAACCTGAAAAGTAGCAGCAGCTGAA 849
QY 802 GATGTTGCAAGCAGTAACCAAAAAGAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 861
Db 850 GATGTTGCAAGCAGTAACCAAAAAGAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 909
QY 862 TGGGAATTCCTGAGTCAAGTTTCATCTCAAGAGAGGAAAACCTGGATGATTGATTGATTGATTGATTGATT 921
Db 910 TGGGAATTCCTGAGTCAAGTTTCATCTCAAGAGAGGAAAACCTGGATGATTGATTGATTGATTGATTGATT 969
QY 922 TTTGCTGTTAAACATCTCCAGATCACAATCTGAAACAGTTTACTCAGACAAAAGGAAAAGAA 981
Db 970 TTTGCTGTTAAACATCTCCAGATCACAATCTGAAACAGTTTACTCAGACAAAAGGAAAAGAA 1029
QY 982 GGAGCATTTATGGTTAGAAAATTCGAGCCCAAGTGGGAATGTACACAGTGTCTTTATTTAGT 1041
Db 1030 GGAGCATTTATGGTTAGAAAATTCGAGCCCAAGTGGGAATGTACACAGTGTCTTTATTTAGT 1089
QY 1042 AAGCTGTGAATGATAAAAAAGGAACCTGTAACAAATTTACCAGTGCATACAATGCTGAG 1101
Db 1090 AAGCTGTGAATGATAAAAAAGGAACCTGTAACAAATTTACCAGTGCATACAATGCTGAG 1149
QY 1102 AACAAATATACCTGGCAGAAAACCTACTGTTTGTATTCCTTCCAAAGCTTATTCATTAT 1161
Db 1150 AACAAATATACCTGGCAGAAAACCTACTGTTTGTATTCCTTCCAAAGCTTATTCATTAT 1209
QY 1162 CATCAACACAAATTCAGCAGGATGATCAACGGGTCCGCCACCTGTGTCAACAGGCC 1221
Db 1210 CATCAACACAAATTCAGCAGGATGATCAACGGGTCCGCCACCTGTGTCAACAGGCC 1269

QY	1222	AACAAGGTCCTCCGACTCTGTGTCCTCTGGGAAATGGAATCTGGGAATCTGGAACATGAAAAGAGAAG	1281
DB	1270	AACAAGGTCCTCCGACTCTGTGTCCTCTGGGAAATGGAATCTGGGAATCTGGAACATGAAAAGAGAAG	1329
QY	1282	ATTACCTTGTGAAGGAGCTGGGAAGTGGCCAGTTTGGAGTGGTCCAGCTGGCGCAAGTGG	1341
DB	1330	ATTACCTTGTGAAGGAGCTGGGAGTGGCCAGTTTGGAGTGGTCCAGCTGGCGCAAGTGG	1389
QY	1342	AAGGGCAGTATGATGTTGCTGTTAAGATGATCAAGGAGGGCTCCATGTGCAGAAAGATGAA	1401
DB	1390	AAGGGCAGTATGATGTTGCTGTTAAGATGATCAAGGAGGGCTCCATGTGCAGAAAGATGAA	1449
QY	1402	TTCTTTTCAGAGGCCAGACTATGATGAAACTCAGCCATCCCANGCTGGTTAAATTCCTAT	1461
DB	1450	TTCTTTTCAGAGGCCAGACTATGATGAAACTCAGCCATCCCANGCTGGTTAAATTCCTAT	1509
QY	1462	GGAGTGTGTTCAAGGAATACCCCATATACATAGTGACTGAATATATAAGCAATGGCTGC	1521
DB	1510	GGAGTGTGTTCAAGGAATACCCCATATACATAGTGACTGAATATATAAGCAATGGCTGC	1569
QY	1522	TTGCTGAAATTACCTGAGGAGTCAGGNAAGGACTTGAACCTTCCAGCTCTTTAGAAATG	1581
DB	1570	TTGCTGAAATTACCTGAGGAGTCAGGNAAGGACTTGAACCTTCCAGCTCTTTAGAAATG	1629
QY	1582	TGCTACGATCTGTGTAAGGCATGGCTTCTTGAGAGTCACCAATTCATACACCGGGAC	1641
DB	1630	TGCTACGATCTGTGTAAGGCATGGCTTCTTGAGAGTCACCAATTCATACCGGGAC	1689
QY	1642	TTGGCTGCTCGTAACCTGCTTGGTGGACAGAGATCTCTGTGTAAGATATCTGACTTTGGA	1701
DB	1690	TTGGCTGCTCGTAACCTGCTTGGTGGACAGAGATCTCTGTGTAAGATATCTGACTTTGGA	1749
QY	1702	ATCACAGGATGTTCTTGATGACCAGTAGTGTCAGTTCAGTCGGACAAAGTTTCCAGTC	1761
DB	1750	ATCACAGGATGTTCTTGATGACCAGTAGTGTCAGTTCAGTCGGACAAAGTTTCCAGTC	1809
QY	1762	AACTGGTTCAGCTCCAGAGTGTGTTCAATTAAGTCAAAATACAGCAGCAAGTCAGACGATGG	1821
DB	1810	AACTGGTTCAGCTCCAGAGTGTGTTCAATTAAGTCAAAATACAGCAGCAAGTCAGACGATGG	1869
QY	1822	GCATTTGGGATTCGTATGTGGGAGGTGTTACGCTTGGGAAAGCAGCCCTATGACTTTGAT	1881
DB	1870	GCATTTGGGATTCGTATGTGGGAGGTGTTACGCTTGGGAAAGCAGCCCTATGACTTTGAT	1929
QY	1882	GACAACCTCCAGCTGCTCTGAAGTCTCCAGGGGCCACAGGCTTTACGGGCCCCACCTG	1941
DB	1930	GACAACCTCCAGCTGCTCTGAAGTCTCCAGGGGCCACAGGCTTTACGGGCCCCACCTG	1989
QY	1942	GCATCGGACACCATCTACCAAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAAAGCGT	2001
DB	1990	GCATCGGACACCATCTACCAAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAAAGCGT	2049
QY	2002	CCACATTTTCAGCAACTCTGCTCCATTTGAACCACTTCGGGAAAAAGACAAAGCATGGA	2061
DB	2050	CCACATTTTCAGCAACTCTGCTCCATTTGAACCACTTCGGGAAAAAGACAAAGCATGGA	2109
QY	2062	AGAAGAAATTTAGAGTTCGTATGAAGATGAATATAGATGCTGGCCAGCATTTTCATTCAT	2121
DB	2110	AGAAGAAATTTAGAGTTCGTATGAAGATGAATATAGATGCTGGCCAGCATTTTCATTCAT	2169
QY	2122	TTTTAAGGAAAGTAGGAAGGCATAAGTAATTTTAGCTAGTTTTTAATAGTGTCTCTCGTAT	2181
DB	2170	TTTTAAGGAAAGTAGGAAGGCATAAGTAATTTTAGCTAGTTTTTAATAGTGTCTCTCGTAT	2229
QY	2182	TGTCCTATATTTAGAAATGAACAAGCAGCGAAACAAAAGATTCCCTTTGAATTTAGATCA	2241
DB	2230	TGTCCTATATTTAGAAATGAACAAGCAGCGAAACAAAAGATTCCCTTTGAATTTAGATCA	2289
QY	2242	AATTAGTAATTTTGTTTTTATGCTGCTCCCTGATATACACTTCCACGCTTATAGCAAGC	2301
DB	2290	AATTAGTAATTTTG -TTTATGCTGCCCTGATATAACACTTCCAGCTTATAGCAAGC 2348	

QY 2302 ACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTTAAAGACTGAGCAG.
DB 2349 ACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGTTAAAGACTGAGCAG.
QY 2362 AATTACTTATTGGATATTCATTCTTTTCTTTATATATGTCATTGTCACAACAACAA
DB 2409 AATTACTTATTGGATATTCATTCTTTTCTTTATATGTCATTGTCACAACAACAA
QY 2422 ACTACCAAGTACAGAAATGTGGAAAAA 2453
DB 2469 ACTACCAAGTACAAAAA 2500

RESULT 5
US-08-391-615-1
: Sequence 1, Application US/08391615
: Patent No. 5550054
: GENERAL INFORMATION:
: APPLICANT: Witte, Owen
: APPLICANT: Tsukada, Satoshi
: APPLICANT: Saifiran, Douglas
: APPLICANT: Rawlings, David
: TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
: TITLE OF INVENTION:
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,615
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/006,449
: FILING DATE: 21-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Rowland, Bertram I
: REGISTRATION NUMBER: 20,015
: REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299 FHT UR
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2505 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 137..2116
: US-08-391-615-1

Db		1005	AAGCTGAGCAACTGCTTAACAGAGAGGGGAAGAAGAGGTTCATTGTGCAGAGACTCCA	1064
Qy		1007	GCCAAAGTGGGAATGTACACAGTGTCCCTTATTTAGTAAGAGGTGTGAATAAATAAGGAA	1066
Db		1065	GCAAAGCTGGAAAATACACCCTGTCTGTGTTTGCTAAATCTACTGGGGAGCCTCAAGGG	1124
Qy		1067	CTGTCAACAATTAACCAAGTGTGATACAATAAGTGTGAGAACAATTAATCTCGCAGAAAACT	1126
Db		1125	TGATCCGCCCATAGTTGTGTGTCTCCACGCCACAGAGCCAGTAGTAATTAOCTGGCTGAGAAAC	1184
Qy		1127	ACTGTTTTGATTCCATTCCAAAGCTTATCATATATCATCAACAATTCACGAGGCATGA	1186
Db		1185	ACCTCTTCAGCACCATCCCTGAGCTCAATTAACCTAACATCAACAACACTCTGCAGGCCCTCA	1244
Qy		1187	TCACAGGCTCCGGCACCTGTGTCAACAAGGCCAACAAAGGTCGCCGACTCTGTGTGCC	1246
Db		1245	TATCCAGGCTGAATATCCTGTCTCTAAACAACAACAAGCGCCCTTCTACTGCAGGCC	1304
Qy		1247	TGGGAATGGAATCTGGGAATCTGAAAGAGAAAGAGATTACTCTTGTGAAGAGACTGGGAA	1306
Db		1305	TGGGCTATGGATCATGGGAATTCATCCAAGGACCTCACCTCTTCAAGAGAGCTTGGGA	1364
Qy		1307	GTGGCCAGTTTGGAGTGGTCCAGCTGGGCAAGTGGGAAGGGGCGAGTAGATGTTGCTGTTA	1366
Db		1365	CTGGCAAAATTCGGTGTCTGTAATATATGGGAAGTGGAGGGGCCAATATGATGTGGCCATCA	1424
Qy		1367	AGATGATCAAGGAGGGCTCCATGCTCAACAAGCATGAATTCWTTTCAGGAGGCCACAGACTGA	1426
Db		1425	AGATGATCAGAGAAGGTTCCATCTCGGAGGATGAATTCATTTGAAGAAGCCAAAGTCAATGA	1484
Qy		1427	TGAACATCAACCCATCCCCAAGCTGGTTAAATTCATATGGAGTGTGTCTCAAGAGAAATACCCCA	1486
Db		1485	TGAATCTTTCCCATTGAGAAGCTGGTGCAGTTGATGGCGCTCGACACAAACAAGCCCCA	1544
Qy		1487	TATACATGTGACTGGAATATATAGAANAATGGCTGCTTCTGCTGAATTAOCTGAGGAGTCAAG	1546
Db		1545	TCCTTCAATCATCCGAGTACATGGCTAATGGCTGCCCTCTTGAOCTACTCTGAGGAGAGATGC	1604
Qy		1547	GAAGAAGCACTTGAACCTTCCAGCTCTTACAAATGTGCTACGATGTCTGTGAAAGCATGG	1606
Db		1605	GGCACCGCTTCCAGACACAGACGCTGCTGAGATGTGCAAGAATGTCTGTGAAGCAATGG	1664
Qy		1607	CCTTCTTTGAGAGTCAACAAATTCATACACGGGACTTGGCTGTGCTGCTGAATCTGTGGTGG	1666
Db		1665	AATACTTTGGAGTCGAAGCAGTTCCCTTCACAGAGACCTGGCAGCTCGAAACTGTTGGTAA	1724
Qy		1667	ACAGAGATCTCTGTGTGAAGTATCTGACTTTTGGAAATGACAAGTATGTTCTTGTATGACC	1726
Db		1725	ACGATCAAGAGTTGTGAAAGTATCTGACTTTGGCCCTGTCTAGGATATGTCCTTGATGATG	1784
Qy		1727	AGTATGTCACTTCAGTCGGGAACAAGPTTCCAGTCAAGTGTGCTGAGTCCAGAGAGTGTTC	1786
Db		1785	AGTACACCACTCTGTAGGCTCAAGPTTCCAGTTCGGTGGTCTCCACCAAGAAGTGTGA	1844
Qy		1787	ATTACTTCAAATACAGCAGCAAGTTCAGACGCTATGGGCAATTTGGGATCCTCATGTGGGAGG	1846
Db		1845	TGTATAGCAAGTTCAGCAGCAAAATCTGACATCTGGGCTTTTGGGTTTTAATGTGGAGA	1904
Qy		1847	TGTTCAAGCTGGGAAGCACGCTTATGACTTGTATGACAACCTCCAGAGTGGTCTCTGAAGG	1906
Db		1905	TCCTACTCCCTTGGGAAGATCCGCTATGAGAGATTTACTAACAGTGAACAGCAGCAAGACCA	1964
Qy		1907	TCCTCCAGGGCCACAGGCTTTTACGGGCCCACTGGCATCTGGGATTTGGGATCCTCATGTGGGAGG	1966
Db		1965	TTGCTCAAGGCTTACGTCTCTACAGGGCTCATCTGGCATCAGAGAGGTATATACCATCA	2024
Qy		1967	TGTACAGCTCTGGCAGGAGCTTCCAGAAAGGCTCCACATTTTCAACAACCTCTCTGTCTT	2026
Db		2025	TGTACAGCTCTGGCAGGAGAAAGCAGATGAAGTCTTAGTTTCAAAATTTCTCTTGAGTA	2084
Qy		2027	CCATTGAACCACTTCGGGAAAAAGA	2051

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DB      2085 ACATTCAGATGTCATGATGAAGA 2109

RESULT 6
US-09-142-529-2
; Sequence 2, Application US/09142529
; Patent No. 6225459
; GENERAL INFORMATION:
; APPLICANT: Mano, Hiroyuki
; APPLICANT: Sakata, Tsuneaki
; APPLICANT: Hasegawa, Mamoru
; TITLE OF INVENTION: Promoter
; FILE REFERENCE: 50026/011001
; CURRENT APPLICATION NUMBER: US/09/142,529
; CURRENT FILING DATE: 1999-08-12
; EARLIER APPLICATION NUMBER: JP 8/54294
; EARLIER FILING DATE: 1996-03-12
; EARLIER APPLICATION NUMBER: PCT/JP97/00741
; EARLIER FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-142-529-2

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Query Match	17.98;	Score 439.4;	DB 3;	Length 2574;
Best Local Similarity	61.5%;	Pred. No. 8.1e-111;		
Matches 723;	Conservative 0;	Mismatches 446;	Indels 6;	Gaps 1;
Qy	899	AAAACCTGGATATGACTGGTTTCTCGTGAACATCTCCAGATCACAATCTGAACAGT	958	
Db	830	ACAACCTTAGATCAATATGAGTGGTACTGCGAAGAAATACCAACAGACGAAAGCAGACAGC	889	
Qy	959	TACTCAGACAAAAGGGGAAAGAGGACATTTATGGTTAGAAATTCGAGCCAAAGTGGGAA	1018	
Db	890	TCCCTCAGAAGGAGATAAAGAGGTGGTTTTATGGTGAGAGACTCCAGTCAACACAGGCT	949	
Qy	1019	TGTACACAGTGTCTTATTTAGTAGAGCTGTGAATGATATAAAAAGGACTGTCAACACTT	1078	
Db	950	TGTACACTGTCTCCCTTTACACAAAGTTTGGGGGAGAGGCTCATCAGSTTTTCAGGCAT	1009	
Qy	1079	ACCAGGTGCA-----TACAAATGCTCAGAACAAATTTATACCTGGCAGAAACTACTGTT	1132	
Db	1010	ATCACATAAGGAACAGCAACATCCCAAGAAGATATTACCTGGCAGACGAACATGCTT	1069	
Qy	1133	TTGATTCCTTCCAAAGCTTTATTCATTATCATCAACACAAATTCAGCAGGCGATGATCACAC	1192	
Db	1070	TCGGGTCCATTCTGTGAGATCATTTGAATATCAACAGCACAAATGCGGCGAGGCTTGTCACCA	1129	
Qy	1193	GGCTCCGCCACCTGTGTCAACAAAGGCCAACAGGTCGCCGACTCTGTGTCCCTCGGAA	1252	
Db	1130	GGCTGCGGATACCCGGTCAGTCAAAAGGGGAGAACGCTCCCACTACTGGCGGCTTCAGCT	1189	
Qy	1253	ATGGAATCTGGGAACCTGAAAGAGAGAGAGATATACCTTGTGAAGGAGCTGGGAAGTGGCC	1312	
Db	1190	ATGATACTGGGAGATTAAACCATCAGAGCTGACCTTTATGAGAGAGTTGGGAGCGGAC	1249	
Qy	1313	AGTTTGGAGTGGTCCAGCTGGGCAAGTGGGAAGGGGCGAGTATGATTTGCTGTTAAGATGA	1372	
Db	1250	TGTTTGGAGTGGTGAAGCTTGGCAAGTGGCGGGCCAGTACAAAGTGGCCATCAAAGCTA	1309	
Qy	1373	TCAAGGAGGCTCCATGCTCAGAAGATGAATTCCTTCAGGAGGCCAGACTATCATGAAAC	1432	
Db	1310	TCCGGGAAGCGCCATGTGTGAGAGAGATTTTCATAGGAAGCTAAAGTCATGATGAAGC	1369	
Qy	1433	TCAGCCATCCAAAGCTGGTAAAATTCCTATGGAGTGTGTTCAAAGGAATACCCCATATACA	1492	
Db	1370	TGACACACCCCAAGCTGGTACAGCTCTATGGTGTATGCACCCAGCAGAGGCCCATCTACA	1429	
Qy	1493	TAGTACTGAATATATAAGCAATGGCTTGCTTGCTGAATTTACCTGAGGAGTCAACGGAAAG	1552	

1430	TCGTTACCGAGTTCATGGAACGGGGCTGCCCTTCTGAATTTCTCCCGCAGAGACAAGGCC	1489
Qy	GACTTGAACCTTCCACGCTCTTGAAGATGTGCTACGATGCTGTGAAGGCATGCCTTCT	1512
Db	ATTTTACCCAGAGACATGCTGCTAAGCATGTGTCAAGATGCTGTGAAGGATGGAGTACC	1549
Qy	TGGAGATCACCAAATTCATACACGGGAGTTGGCTGCTCGTAACTGCTTGGTGGACAGAG	1572
Db	TGGAGAGAAACTTCTTCATCCACAGAGACCTGGTGCACAGAAATGTCTAGTGAATCAAG	1609
Qy	ATCTCTGTGTCAAGATATCTGACTTTTGGAAATGACAAGGTATGTCTTGATGACCAAGTATG	1732
Db	CAGAGTGTGCAAGTATCTGATTTTGGAAATGGCCAGGTACGTTCTGGATGATCAGTACA	1669
Qy	TCAGTTTCAGTCCGGAACCAAGCTTTCCAGTCAAGTGGTCAGCTCCAGAGGCTGTTTCATTACT	1792
Db	CAAGTCTCTTTCGGCCCAAGTTCCCTGTGAAGTGGTGTCCCCACAGAAGTGTTTAAATTACA	1729
Qy	TCAAAATACAGCAGCAAGTCAGACGTATGGGCATTTGGGATCCTGATGTGGAGGCTGTCA	1852
Db	CGCGCTTTAGCAGCAAGTCAGACGTCTGGTCGTTTGGTGTGCTAAATGTGGGAAATATCA	1789
Qy	GCCTGGGACAGCAGCCCTATGACTTGTATGCACAACTCCAGTGGTGTCTGAAGTCTCCC	1912
Db	CAGAAGCGAGGATGCCCTTTTGAGAAGAACAACCAATTACGAAGTGGTAACCATGTGACTC	1849
Qy	AGGGCACACGGCTTTTACCGCCCCACCTGGCATCGGACACCACTACCAGATCATGTACA	1972
Db	GTGGCCACCCCTCCACCGGCCCAAGCTGGCTTCCAAATATTTGTATGAGGTCATGCTGA	1909
Qy	GCTGCTGGCACGAGCTTTCAGAAAAAGCGTCCACATTTTACGAACCTCCCTGCTTCCATTG	2032
Db	GATGCTGGCAAGAGACAGAGGGAAGGCCCTTCCCTTTGNAGACTTGCTGCGTACGATAG	1969
Qy	AACCACTTCGGGAAAAAGACAAGCATTTGAAGAAGA	2067
Db	ATGAACATGATTGAATGTGAAGAACTTTTTCGAAGA	2004

RESULT 7

```

US-10-045-428A-2
; Sequence 2, Application US/10045428A
; Patent No. 6500943
; GENERAL INFORMATION:
; APPLICANT: Mano, Hiroyuki
; APPLICANT: Sakata, Tsuneaki
; APPLICANT: Hasegawa, Mamoru
; APPLICANT: Tabata, Toshiaki
; TITLE OF INVENTION: Promoter
; FILE REFERENCE: 50026/031003
; CURRENT APPLICATION NUMBER: US/10/045,428A
; CURRENT FILING DATE: 2002-04-15
; PRIORITY APPLICATION NUMBER: 09/735,103
; PRIORITY FILING DATE: 2000-12-12
; PRIORITY APPLICATION NUMBER: 09/442,529
; PRIORITY FILING DATE: 1999-08-12
; PRIORITY APPLICATION NUMBER: PCT/JP97/00741
; PRIORITY FILING DATE: 1997-03-10
; PRIORITY APPLICATION NUMBER: JP 8/54294
; PRIORITY FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-045-428A-2

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Query Match 17.9%; Score 439.4; DB 4; Length 2574;
Best Local Similarity 61.5%; Pred. No. 8,1e-111;
Matches 723; Conservative 0; Mismatches 446; Indels 6;

QY 899 AAAACCTGGATGATTATGACTGGTTTGGTGGTAACATCTCCAGATCACAATCTGAACAGT 958

Db 1910 GATGCTGGCAAGAGAGACAGAGGAGGAGGCTTCTTCTTGAAGACTTGTCTGCTACGATAG 1969
QY 2033 AACCACTTCGGGAAAGACAGACATTCAGCAAGA 2067
Db 1970 ATGAACAGTGTGAATGTGAAGAACTTTTGAAGA 2004

RESULT 8
US-08-306-691B-35
; Sequence 35, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-306-691B-35

Query Match 9.0%; Score 220.2; DB 1; Length 3623;
Best Local Similarity 52.9%; Pred. No. 2e-50;
Matches 521; Conservative 0; Mismatches 458; Indels 6; Gaps 2;

QY 1061 AAGGAAGCTCAACATTACACCTGGATACAAATGCTGGAAACAATATACCTGGCAG 1120
Db 650 AAGGAGGGTGTACATTACAGGATCAACATGCTGTGTGATGGCAAGCTCTACGTCCT 709
QY 1121 AAAAAGTCTGTTTGTATCCATTCCAAAGCTTATTCATTCATCAACACAATTCAGCAG 1180
Db 710 CCGAGAGCCGCTTCAACACCTGCGGAGTTGGTTTCATCATTCATCAACGGTGGCCGACG 769
QY 1181 GCATGATCACAGGCTCGGCACCCCTGTGTCAACAAGGCCAACAAGTCCCGCACTCTG 1240
Db 770 GGCTCATCACACGCTCCATTATCCAGCCCAAGGCAACAAGCCCACTGTCTATGTG 829
QY 1241 TGTCCTCGGGAATGGATCTGGGAATCAAGAGAGAGATTCCTTGTGGAAGGAC 1300
Db 830 TGTCCTCGGGAATGGATCTGGGAATCAAGAGAGATTCCTTGTGGAAGGAC 889
QY 1301 TGGGAAGTGGCCAGCTTTGGAGTGTGCCAGCTGGGCAAGTGGAGGGGCA---GTATGATG 1357

RESULT 9

US-09-220-132-77

; Sequence 77, Application US/09220132

; Patent No. 6506607

; GENERAL INFORMATION:

; APPLICANT: Shyian, Andrew W.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT

; FILE REFERENCE: 07334-074001

; CURRENT APPLICATION NUMBER: US/09/220,132

; CURRENT FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: US 60/079,303

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: US 60/068,821

; PRIOR FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 77

; LENGTH: 2647

; TYPE: DNA

; ORGANISM: Homo sapiens

Db 890 TGGCGGGGGCCAGTACGGGGAGGTGTACGAGGGCGTGTGGAAGAAATACAGCCTGCACGG 949
QY 1358 TTGCTGTTAAGATGATCAAGGAGGCTCCATGTCAGAAGATGAATTCCTTTAGGAGGGCCC 1417
Db 950 TGGCGGTGAAGACCTTGAAGGAGGACACCATGGAGTGGAGAGGTCTTTGAAGAAGCTG 1009
QY 1418 AGACTATGATGAACACTCAGCCATCCAAAGCTGGTTAAATTCATGAGTGTCTTCAAAGG 1477
Db 1010 CAGTCATGAAGAGATCAACACCCCTAACCTAGTCAGCTCCTTGGGGTCTCCACCCGG 1069
QY 1478 AATACCCCATATACATAGTGTACTATATATAAGCAATGGCTGTCTTGTGAATTAACCTGA 1537
Db 1070 AGCCCCCGTCTATATCATCTAGTTCATGACCTACGGGAACCTCCTGGACTACCTGA 1129
QY 1538 G---GAGTCACGGAAGAGACTTGAACCTTCCAGCTCTTAGAAATGCTCAGATGTCT 1594
Db 1130 GGGAGTGAACCGCGGAGGAGGTGAACGCGGTGCTGCTGTACATGGCCACTCAGATCT 1189
QY 1595 GTGAAGCATGCCCTTCTTGGAGAGCTCACCATTATACACGGGACTTGGCTGCTCGTA 1654
Db 1190 CGTCAGCCATGGAGTACCTAGAGAAGAAACCTTCATCCACAGATCTTGTGCCCCGAA 1249
QY 1655 ACTGCTTGGTGACAGAGATCTCTGTGAAAGTATCTGACTTTGGAATGACAAGTATG 1714
Db 1250 ACTGCTGTTAGGGGAGAACCACTTGTGAGGTAGCTGATTTTGGCCTGACAGGTGA 1309
QY 1715 TTCTTGATGACAGTATGTCTAGTTCAGTCGGGAACAAAGTTTCCAGTCAAGTGTGACGTC 1774
Db 1310 TGACAGGGGACACCTTACACAGCCCATGCTGGAGCCAAAGTTCCCCATCAATGGACTGCAC 1369
QY 1775 CAGAGTCTTTCATTACTTCAATACAGCAGCAAGTCAAGCTATGGGCAATTTGGCATCC 1834
Db 1370 CCGAGAGCTGGCCTTACAAACAAGTTCTCATCAAGTCCAGCTCTGGGCAATTTGGAGTAT 1429
QY 1835 TGATGTGGGAGGTGTTAGCCTGGGAAGCAGCCCTATGACTTGTATGACAACCTCCAGG 1894
Db 1430 TGTCTTGGGAAATTCCTACCTATGTCATGCTCCCTTACCCGGGAATTGACCGTTCCAGG 1489
QY 1895 TGGTTCGAAGTCTCCAGGGCCACAGGCTTTACGGCCCCACCTGGGCAATTTTCAGC 1954
Db 1490 TGATGAGTCTGTAGAGAAGGACTACCGCATGAAGCGCCCAAGGCTGCCCAAGAGG 1549
QY 1955 TCTACCATCATGTACAGCTGCTGGCAGAGCTTCCAGAAAAGCTCCACATTTTCAGC 2014
Db 1550 TCTATGAACCTATCGGAGCATGTTGGCAGTGAATCCCTCTGACCGCCCTCCTTTGCTG 1609
QY 2015 AACTCTGTCTTCCATTGAACCACT 2039
Db 1610 AATCCACCAAGCCCTTGAACAAT 1634

US-09-220-132-77

Query Match 8.6%; Score 211.6; DB 4; Length 2647;
Best Local Similarity 52.3%; Pred. No. 4e-48;
Matches 516; Conservative 0; Mismatches 464; Indels 6;

[illegible]

1520	Db	1520	AAGCGCAGATCATGAAGAAGCTGAAGCAGCAGCAAGCTGGTCCAGCTCTATGCAAGTGGTGT	1579
1472	Qy	1472	CAAAAGGAAATACCCCATATACATAGTGAATATATATGAACAATGGCTGCTGCTGAAAT	1531
1580	Db	1580	CTGAGG---AGCCCATCTACATCGTCACCGAGTATATGAACAAGGAAGTTTACTGGATT	1636
1532	Qy	1532	ACCTGA---GGAGTACGAGAAAGGACTTGAACCTTCCCGAGCTTCTTGAANAATGTGTACG	1588
1637	Db	1637	TCTTAAAGATGAGGAAGGAAGAGCTCTGAAATATGCAAAATCTGTGGACATGGCAGCAC	1696
1589	Qy	1589	ATGCTGTGAAGCATTGGCTTCTTGGAGAGTCACCAATTCATACACCGGAGCTTGGCTG	1648
1697	Db	1697	AGGTGGCTGCAGGAATGGCTTACATCAGCGCATGAATATATATCCATAGAGATCTCGGAT	1756
1649	Qy	1649	CTCGTAACCTGCTTGGTGGACAGAGATCTCTGTGTGAAAGTATCTGACTTTTGGAAATGACAA	1708
1757	Db	1757	CAGCAAAACATTCCTAGTGGGGAATGGACTCATATGCAAGATTGCTGACTTCGGATTGGCCC	1816
1709	Qy	1709	GGTATGTTCTTGATGACCAGATGTGAGTTCAGTCACTCGGAACAAGTTTCCAGTCAAGTGGT	1768
1817	Db	1817	GATTGTATGAAGACAATGAGTATACACAGCAAGCAAGGTGCAAGTTTCCCATCAAGTGGGA	1876
1769	Qy	1769	CAGCTCCAGAGGTGTTTCATTACTTCAAAATACAGCAGCAAGTCAGACGTAATGGGCATTTG	1828
1877	Db	1877	CGCCCCCGAGGCGCCCTGTACGGGAGGTTCACATCAAGTCTGACGTGTGCTCTTTTG	1936
1829	Qy	1829	GGATCTGATGTGGGAGGTGTTTCAGCCTGGGGAGCAGCCCTATGACTTGTATGACAACAT	1888
1937	Db	1937	GAATCTTTACTTCACAGAGCTGGTCACCAAAAGGAAGAGTGGCCATACCCAGGCGATGAACAACC	1996
1889	Qy	1889	CCAGTGGTCTTCGAGGTCTCCACAGGGCCACAGGCTTACCGGCCCCACCTGGCATCGG	1948
1997	Db	1997	GGAGGTGCTTGGAGCAGGTGGAGCGAGGTACAGGATGGCTTCCCGCAGGAGTGGCCCCA	2056
1949	Qy	1949	ACACCATCTACCAAGATCATAGACGTGTGGCAGCAGAGCTTCCAGAAAAACGGTCCACAT	2008
2057	Db	2057	TCTCTCTGATGAGCTCATGATCCACTGCTGGAAAAGGACCCCTGAAAGACGCCCACTT	2116
2009	Qy	2009	TTCAGCAACTCCCTGCTTCCATTGAA	2034
2117	Db	2117	TTGAGTACTTGCAGAGCTTCTCTGGAA	2142

RESULT 11

RESOLV 11
US-08-391-615-7
Sequence 7, Application US/08391615
Patent No. 5550054
GENERAL INFORMATION:
APPLICANT: Witte, Owen
APPLICANT: Tsukada, Satoshi
APPLICANT: Saffran, Douglas
APPLICANT: Rawlings, David
TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/391,615
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/006,449


```

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 255 1401
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1602 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gallus, gallus
; PUBLICATION INFORMATION:
; AUTHORS: Takeya, Tatsuo
; TITLE: Structure and Sequence of the
; TITLE: Cellular Gene Homologous to the RSV src
; TITLE: Gene and the Mechanism for Generating the
; TITLE: Transforming Virus
; JOURNAL: Cell
; VOLUME: 32
; PAGES: 881-890
; DATE: March, 1983
;
; US-07-820-011A-1
;
Query Match      8.3%; Score 204; DB 1; Length 1602;
Best Local Similarity 55.8%; Pred. No. 3.7e-46;
Matches 450; Conservative 0; Mismatches 350; Indels 6; Gaps 3;

QY 1231 CCGGACTCTGTGCTGCGGAAATGGAATCTGGGAAGTAAAGAGAGAGAGAGATTTACCTTG 1290
Db 1231 CCGGACTCTGTGCTGCGGAAATGGAATCTGGGAAGTAAAGAGAGAGAGAGATTTACCTTG 1290
QY 1291 TTGAAGAGCTGGAGAGTGGCCAGTTTGGAGTGTCCAGCTGGGCAAGTGAAGGGCAG 1350
Db 1291 TTGAAGAGCTGGAGAGTGGCCAGTTTGGAGTGTCCAGCTGGGCAAGTGAAGGGCAG 1350
QY 1351 TATGATGTTCTGTTAGATGATCAAGGAGGCTCCATGTCAGAGATGAATTTTCAG 1410
Db 1351 TATGATGTTCTGTTAGATGATCAAGGAGGCTCCATGTCAGAGATGAATTTTCAG 1410
QY 1411 GAGGCCAGACTATGATGAAGTCAAGCTCCCAAGCTGTTAAATCTATGAGTGTGT 1470
Db 1411 GAGGCCAGACTATGATGAAGTCAAGCTCCCAAGCTGTTAAATCTATGAGTGTGT 1470
QY 1471 TCAAGGAATACCCCATATACATAGTACGTGAATATATAGCAATGCTGCTGCTGAAT 1530
Db 1471 TCAAGGAATACCCCATATACATAGTACGTGAATATATAGCAATGCTGCTGCTGAAT 1530
QY 1531 TACCTGA--GGAGTACGGAAAGAGACTTGAACCTTCC--CAGCTCTTAGAAATGTGCTAC 1587
Db 1531 TACCTGA--GGAGTACGGAAAGAGACTTGAACCTTCC--CAGCTCTTAGAAATGTGCTAC 1587

1045 TTCTGAAGGAGAGATGGCAAGTACCTTGGGCTGCCACACACACTCGTCATATGCTGCT 1104
1588 GATGCTCTGTAAGGATGGCTTCTTGGAGAGTACCACAAATTCATACACGGAGCTTGGCT 1647
1105 CAGATTGTCATCCGGCATGGCTTATCTGGAGAGAGTGAACCTACGTCACCGAGACCTGCGG 1164
1648 GCTCGTAACTGCTTGGTGGACAGAGATCTCTCTGTGAAAAGTATCTGACTTTTGAATGACA 1707
1165 GCGGCAACATCCTTGGTGGGAGAACCTGTGTCAAGGTGGTACTTTGGGCTGGCA 1224
1708 AGGTATGTTCTGTATGACACAGTATGTCAGTTTCAGTCGGAACAAAGTTTCCAGTCAAGTGG 1767
1225 GCGCTCATCGAGGACACAGAGTACACACAGCGGCAAGGTGCCAAGTTCCTCCATCAAGTGG 1284
1768 TCAGCTCCAGAGGTGTTTTCATTACTTCAATACAGCAGCAAGTTCAGACGTATGGGCAATT 1827
1285 ACAGCCCCGAGGAGCGCTCTATGCGCGGTTTCAACCATCAAGTCGATCTCTGTCCTTC 1344
1828 GGGATCCTGATGTTGGGAGGTGTTTCAAGTCTCCAGGCGCACAGGCTTTACCGGCCCCCAGCTGGCATCG 1947
1345 GGCATCCTGCTGACTGAGCTGACCTGACCAAGGCGCGGTGCCATACCCAGGAGTGGTCAAC 1404
1888 TCCAGGTGTTCTGAAGTCTCCAGGCGCACAGGCTTTACCGGCCCCCAGCTGGCATCG 1947
1405 AGGAGGTGCTGGACCAAGTGGAGAGGCTTACCGCTGCCCGCCGAGTGGCCCC 1464
1948 GACACCATCTACAGATCATGTACAGCTGTGGCAGCAGCTTCCAGAAAGGCTGCCACA 2007
1465 GAGTCGCTGTCATGACCTCATGTGCCAGTGTGCGGAGGAGGAGCCCTGAGAGCGGCCACT 1524
2008 TTTGAGTACCTGCTGCTTCCATTGA 2033
1525 TTTGAGTACCTGCGAGGCTTCTCTGGA 1550

RESULT 15
PCT-US93-00445-1
; Sequence 1, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:

LENGTH: 1602 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Gallus, gallus

PUBLICATION INFORMATION:

AUTHORS: Takeya, Tatsuo

TITLE: Hanafusa, Hidesaburo

TITLE: Structure and Sequence of the

TITLE: Cellular Gene Homologous to the RSV src

TITLE: Gene and the Mechanism for Generating the

TITLE: Transforming Virus

JOURNAL: Cell

VOLUME: 32

PAGES: 881-890

DATE: March, 1983

PCT-US93-00445-1

Query Match

Best Local Similarity 55.8%; Pred. No. 3.7e-46;

Matches 450; Conservative 0; Mismatches 350; Indels 6; Gaps 3;

QY 1231 CCGACTCTGTGCCCTGGGAATGGAATCTGGAACTGAAAGAGAGATTACCTTG 1290

Db 748 CCGAGACCCAGGAGCTCGCAAGAGCGCTGGGAAATCCCGGGAGCTGCTGGCTG 807

QY 1291 TTGAAGAGCTGGAGTGTGGAGTGTCCAGCTGGCAAGTGGAGGGGAGGCGCAG 1350

Db 808 GAGGTGAAGCTGGGGAGGCTGCTTTGGAGAGTCTGGATGGGGAGCTGGAACGGCACC 867

QY 1351 TATGATGTTCTTAAAGATGATCAAGAGGGGTCCATGTGCAAGAGATGAATTTTCAG 1410

Db 868 ACCAGAGTGGCCATAAGACTCTGAAGCCCGGCAACATGTCCCGGAGGCTTCTCTCAG 927

QY 1411 GAGGCCAGACTATGATGAAGTCAAGCTCCCAAGCTGGTTAAATTTCTATGGAGTGTG 1470

Db 928 GAAGCCCAAGTGAAGAAGCTCCGCGCATGAGAAGCTGTTACGCTGTACGCAAGTGGT 987

QY 1471 TCAAGGAATACCCATATACATGACTGACTGAATATATAGCATGCTGCTTCTGCTGAAT 1530

Db 988 TC---GGAAGAGCCCATCTACATCGTCACTGAGTACATGAGCAAGGGGAGGCTCCTGGAT 1044

QY 1531 TACCTGA--GGAATCAGGAAAGGACTTGAACCTTCC--CAGCTCTTTAGAAATGTGCTAC 1587

Db 1045 TTCTGAAGGAGAGATGGCAAGTACCTGGGCTGCCACAGCTCGTGATATGGCTGCT 1104

QY 1588 GATGCTGTGAAGCATGGCTTCTGGAGAGTCAACAAATTCATACACCGGGAGCTTGGCT 1647

Db 1105 CAGATTGCATCCGGCATGGCTATGTGGAGAGGATGAACACTACGTGCACCGAGAGCTGGG 1164

QY 1648 GCTCGTAACCTGTGGTGGACAGAGATCTGTGTGAAGTATCTGACTTTGGATGACA 1707

Db 1165 GCGGCCAACATCTGTGGGGGAGAACCTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCA 1224

QY 1708 AGGTATGTTCTGTGATGACCATGATGTGAGTTAGTTCGGAACAAAGTTTCCAGTCAAGTGG 1767

Db 1225 CGCTCATCGGACACAGGATACACAGCAGCGCAAGGTGCCAAGTTCCCATCAAGTGG 1284

QY 1768 TCAGTCCAGAGGTGTTTACTTCAATATACAGCAGCAAGTCAAGTCAAGTATGGGCAATT 1827

Db 1285 ACAGCCCCGAGGAGCGCCCTATGCGCGGTTCACCATCAAGTCGGATGTCTGTCCTTC 1344

QY 1828 GGGATCTGTATGTTGGAGTGTTCAGCTGGGGAGCAGCCCTATGACTTGTATGACAAC 1887

Db 1345 GGCATCTGTGATGAGTGACCAACCAAGGCGCGGTGCCATACCCAGGGAGTGTCAAC 1404

QY 1888 TCCAGGTGTTCTGAAGGTCTCCAGGGGACAGAGGCTTTACCGGCCCCACCTGGCATCG 1947

Db 1405 AGGAGGTGCTGGACCAGAGTGGAGGGGCTACCGCATGCCCTGCCCGCCGAGTGGCCCC 1464

QY 1948 GACACCATCTACAGATCATGTACAGCTGTGGCAGGCTTCCAGAAAAAGCGTCCCAACA 2007

Db 1465 GAGTCGCTGCATGACCTCATGTGCGCATGTGGGAGGAGGACCTTGAGGAGCGGCCACT 1524

QY 2008 TTTCAGCAACTCCCTGTCTTCCATTGA 2033

Db 1525 TTTGAGTACCTGCAGGCGCTTCTCTGGA 1550

Search completed: August 20, 2003, 16:30:06
Job time : 170 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 15:10:22 ; Search time 556 Seconds

(without alignments)
9930.738 Million cell updates/sec

Title: US-10-021-660-41

Perfect score: 2456

Sequence: 1 gcaagcagcagcaagctga.....aatgtggaataaaacacg 2456

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0.

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2456	100.0	2456	12	US-10-021-660-41
2	2456	100.0	2456	12	Sequence 41, Appl
3	2424.4	98.7	2419	11	Sequence 1, Appl
4	2404.2	97.9	2604	14	US-10-171-581-317
5	2397.6	97.6	2500	9	US-09-977-269-3
6	2397.6	97.6	2500	10	US-09-977-260-3
7	2397.6	97.6	2500	11	US-09-977-261-3
8	650.8	26.5	797	11	US-09-955-999-27
9	494.6	20.1	2468	14	US-10-045-202-3
10	485	19.6	2560	14	US-10-045-202-1
11	480.2	19.6	2582	14	US-10-220-801-4
12	439.4	17.9	2574	9	US-09-735-103-2
13	439.4	17.9	2574	13	US-10-045-428A-2
14	394.4	16.1	3663	10	US-09-919-172-84
15	388	15.8	3593	14	US-10-220-801-6
16	385.4	15.7	4221	14	US-10-220-801-8

17	385.4	15.7	6383	10	US-09-954-531-405	Sequence 405, App
18	383.8	15.6	6381	12	US-10-007-928A-45	Sequence 45, Appl
19	263.4	10.7	431	14	US-10-106-698-1335	Sequence 1335, Ap
20	223.4	9.1	5527	10	US-09-880-107-3710	Sequence 3710, Ap
21	211.6	8.6	4414	12	US-10-101-510-512	Sequence 512, App
22	208	8.5	347	10	US-09-833-381-1818	Sequence 1818, Ap
23	208	8.5	347	10	US-09-833-381-1819	Sequence 1819, Ap
24	191.4	7.8	2354	10	US-09-967-768A-300	Sequence 300, App
25	189.2	7.7	2015	10	US-09-954-456-1983	Sequence 1983, Ap
26	189.2	7.7	2015	14	US-10-007-010-3	Sequence 3, Appl
27	181.2	7.4	2298	14	US-10-175-523-50	Sequence 50, Appl
28	178	7.2	1911	10	US-09-917-800A-1611	Sequence 1611, Ap
29	168	6.8	2770	9	US-09-977-269-5	Sequence 5, Appl
30	168	6.8	2770	10	US-09-977-260-5	Sequence 5, Appl
31	168	6.8	2770	11	US-09-977-261-5	Sequence 5, Appl
32	168	6.8	2863	10	US-09-954-456-1691	Sequence 1631, Ap
33	168	6.8	7607	10	US-09-982-610-19	Sequence 19, Appl
34	160.2	6.5	454	11	US-09-918-995-26678	Sequence 20678, A
35	159	6.5	462	9	US-09-864-767-5598	Sequence 5598, Ap
36	158.8	6.5	347	10	US-09-796-692-8836	Sequence 8836, Ap
37	158.8	6.5	347	14	US-10-040-622A-6	Sequence 6, Appl
38	157.6	6.4	774	11	US-09-956-622A-6	Sequence 304, App
39	153	6.2	4517	12	US-10-007-926A-304	Sequence 3, Appl
40	153	6.2	4517	15	US-10-298-377A-3	Sequence 11293, A
41	148.2	6.0	452	9	US-09-864-761-11293	Sequence 1, Appl
42	142.6	5.8	2674	13	US-10-003-295-1	Sequence 4, Appl
43	138.4	5.6	2451	10	US-09-771-161A-4	Sequence 12, Appl
44	136.2	5.5	1574	9	US-09-870-962-12	Sequence 15, Appl
45	134	5.5	159	11	US-09-158-722-15	

ALIGNMENTS

RESULT 1

US-10-021-660-41
: Sequence 41, Application US/10021660
: Publication No. US20030152926A1
: GENERAL INFORMATION:
: APPLICANT: Murray, Richard
: APPLICANT: Glynnne, Richard
: APPLICANT: Watson, Susan R.
: APPLICANT: EOS Biotechnology, Inc.
: TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
: TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
: FILE REFERENCE: 018501-00071005
: CURRENT APPLICATION NUMBER: US/10/021,660
: CURRENT FILING DATE: 2001-12-06
: PRIOR APPLICATION NUMBER: US/09/784,356
: PRIOR FILING DATE: 2001-02-14
: PRIOR APPLICATION NUMBER: US/09/637,977
: PRIOR FILING DATE: 2000-08-11
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 41
: LENGTH: 2456
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-021-660-41

Query Match	100.0%	Score 2456;	DB 12;	Length 2456;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches:2456;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	GCACGACGGACACAGCTGACGCGATGATATATGATACACAAATCTATTCTAGAGAA	60	
Db	1	GCACGACGGACACAGCTGACGCGATGATATGATACACAAATCTATTCTAGAGAA	60	
Qy	61	CTTCTTCTTCAAAAGATCACAGCAAAAGAGAAATGTCACCAATAATTTACAAAGACGG	120	
Db	61	CTTCTTCTTCAAAAGATCACAGCAAAAGAGAAATGTCACCAATAATTTACAAAGACGG	120	

QY 121 CTTTTGTTTGGACCAAAACAACTTTCTACTATGAATATGACAAAATGAAAGGGGC 180
DB 121 CTTTTGTTTGGACCAAAACAACTTTCTACTATGAATATGACAAAATGAAAGGGGC 180
QY 181 AGCAGAAAAGGATCCATTGAAATTAAGAAATCAGATGTGTGGAGAAATGAATCTCGAG 240
DB 181 AGCAGAAAAGGATCCATTGAAATTAAGAAATCAGATGTGTGGAGAAATGAATCTCGAG 240
QY 241 GAGCAGCGCTGTAGACAGACAGTACCATTTCAGATTGCTATATAAGAGTGGGCTTCTC 300
DB 241 GAGCAGCGCTGTAGACAGACAGTACCATTTCAGATTGCTATATAAGAGTGGGCTTCTC 300
QY 301 TATGTCTATGCATCAAAATGAAGAGCGCGAAGTCAAGTGTTCGAGCAATTCATGAGTCTTC 360
DB 301 TATGTCTATGCATCAAAATGAAGAGCGCGAAGTCAAGTGTTCGAGCAATTCATGAGTCTTC 360
QY 361 ATAAGGGGTAAACCCCACTGCTGTCAAGTACCATAGTGGGTTCTTGGTGACGGGAAG 420
DB 361 ATAAGGGGTAAACCCCACTGCTGTCAAGTACCATAGTGGGTTCTTGGTGACGGGAAG 420
QY 421 TTCCTGTGTTGCCAGCAGAGCTGTAAAGCAGCCCGAGGATGTACCCTCTGGGAACATAT 480
DB 421 TTCCTGTGTTGCCAGCAGAGCTGTAAAGCAGCCCGAGGATGTACCCTCTGGGAACATAT 480
QY 481 GCTAATCTGCATCTGCAAGTCAATGAAGAGAAACACAGAGTTCACACCTTCCAGACAGA 540
DB 481 GCTAATCTGCATCTGCAAGTCAATGAAGAGAAACACAGAGTTCACACCTTCCAGACAGA 540
QY 541 GTGCTGAAGATACCTTCGGGCGAGTTCCTGTTCTCAAAATGGATGCACCATCTTCAAGTACC 600
DB 541 GTGCTGAAGATACCTTCGGGCGAGTTCCTGTTCTCAAAATGGATGCACCATCTTCAAGTACC 600
QY 601 ACTCTAGCCCAATATGACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCATCTTCA 660
DB 601 ACTCTAGCCCAATATGACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCATCTTCA 660
QY 661 AGTACCAGTCTAGGCGCAATATGACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCAT 720
DB 661 AGTACCAGTCTAGGCGCAATATGACAGCAACTCAAGAAAATCTATGGCTCCAGCCACCAT 720
QY 721 TTCACATGAGTATATTCAGGGAAGACTTCCCTGACTGGTGGCAAGTAAAGAAATCTG 780
DB 721 TTCACATGAGTATATTCAGGGAAGACTTCCCTGACTGGTGGCAAGTAAAGAAATCTG 780
QY 781 AAAAGTACGACGAGTGAAGATGTTGCAAGCAGTAAACAAAAGAAAGAAATCTGGAAT 840
DB 781 AAAAGTACGACGAGTGAAGATGTTGCAAGCAGTAAACAAAAGAAAGAAATCTGGAAT 840
QY 841 CACACCACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAA 900
DB 841 CACACCACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAA 900
QY 901 AACCTGGATGATATGACTGGTGGTACATCTCCAGATCAATCTGAACAGTTA 960
DB 901 AACCTGGATGATATGACTGGTGGTACATCTCCAGATCAATCTGAACAGTTA 960
QY 961 CTCAGAAAAAGGAAAAAGAGGAGCATTTATGTTAGAAATTCGAGCCAAAGTGGGAATG 1020
DB 961 CTCAGAAAAAGGAAAAAGAGGAGCATTTATGTTAGAAATTCGAGCCAAAGTGGGAATG 1020
QY 1021 TACACAGTCTCTTATTTAGTAAAGCTGTGAATGATAAAAAAGGAACGTCAAAACATTTAC 1080
DB 1021 TACACAGTCTCTTATTTAGTAAAGCTGTGAATGATAAAAAAGGAACGTCAAAACATTTAC 1080
QY 1081 CACGTGCATCAAAATGCTGAGAACAAATATACCTGGCAGAAACTACTGTTTTGATTTCC 1140
DB 1081 CACGTGCATCAAAATGCTGAGAACAAATATATACCTGGCAGAAACTACTGTTTTGATTTCC 1140
QY 1141 ATTCGAAGCTTATTCATTTATCATCAACACATTCAGCAGCGATGATCACAGGCTCCGC 1200
DB 1141 ATTCGAAGCTTATTCATTTATCATCAACACATTCAGCAGCGATGATCACAGGCTCCGC 1200
QY 1201 CACCTGTGTCAACAAAGGGCCAAAGGTGCCGACTCTGTCTCCCTGGGAAATGGAATC 1260

DB 1201 CACCTGTGTCAACAAAGGGCCAAAGGTGCCGACTCTGTCTCCCTGGGAAATGGAATC 1260
QY 1261 TGGGAACCTGAAAGAGAGAGATTAACCTTGTGTAAGGAGCTGGGAAGTGGCCAGTTGGA 1320
DB 1261 TGGGAACCTGAAAGAGAGAGATTAACCTTGTGTAAGGAGCTGGGAAGTGGCCAGTTGGA 1320
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DB 1321 GTGGTCCAGCTGGGCAAGTGGAGGGGAGTATGATGTTGCTGTTAAAGATGATCAAGGAG 1380
QY 1381 GSCTCCATGTCAGAGATGAATTTCTTTCAGGAGGCCAGACTATGATGATAAATCAACCAT 1440
DB 1381 GSCTCCATGTCAGAGATGAATTTCTTTCAGGAGGCCAGACTATGATGATAAATCAACCAT 1440
QY 1441 CCCAAGCTGGTTAAATTTCTATGAGTGTGTTCAAAGGAATACCCCATATACATAGTACT 1500
DB 1441 CCCAAGCTGGTTAAATTTCTATGAGTGTGTTCAAAGGAATACCCCATATACATAGTACT 1500
QY 1501 GAATATATAAGCAATGGCTGCTGCTGAATTAACCTGAGGAGTCAACGAAAAGGACTTGAA 1560
DB 1501 GAATATATAAGCAATGGCTGCTGCTGAATTAACCTGAGGAGTCAACGAAAAGGACTTGAA 1560
QY 1561 CTTCCCACTCTTAGAAAATGCTACGATGCTGTGAAGGATGCGCTTCTTGGAGAGT 1620
DB 1561 CTTCCCACTCTTAGAAAATGCTACGATGCTGTGAAGGATGCGCTTCTTGGAGAGT 1620
QY 1621 CACCAATTCATACACGGGAGCTTGGCTGCTGTAAGTCTGTTGGTGACAGAGATCTCTGT 1680
DB 1621 CACCAATTCATACACGGGAGCTTGGCTGCTGTAAGTCTGTTGGTGACAGAGATCTCTGT 1680
QY 1681 GTGAAGTATCTGACTTTGGGAATGACAAGTATGTTCTTGTGACCAAGTATGTCAGTTCA 1740
DB 1681 GTGAAGTATCTGACTTTGGGAATGACAAGTATGTTCTTGTGACCAAGTATGTCAGTTCA 1740
QY 1741 GTCGGAACAAAGTTTCCAGTCAAGTGGTCCAGCTCCAGAGTGTGTTTCAATTTCAATAC 1800
DB 1741 GTCGGAACAAAGTTTCCAGTCAAGTGGTCCAGCTCCAGAGTGTGTTTCAATTTCAATAC 1800
QY 1801 AGCAGCAAGTCAGAGCTATGGGCATTTGGGATCTCTGATGTTGGAGTGTTCAGCCTGGG 1860
DB 1801 AGCAGCAAGTCAGAGCTATGGGCATTTGGGATCTCTGATGTTGGAGTGTTCAGCCTGGG 1860
QY 1861 AAGCAGCCTATGACTTGTATGACAACTCCAGGTGTTCTGAAGTCTCCAGGCGCAC 1920
DB 1861 AAGCAGCCTATGACTTGTATGACAACTCCAGGTGTTCTGAAGTCTCCAGGCGCAC 1920
QY 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCATCTACAGATCATGTGTACAGTCTGTG 1980
DB 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCATCTACAGATCATGTGTACAGTCTGTG 1980
QY 1981 CACGAGCTTCCAGAAAAGCGTCCACATTTTCAGCACTCTGCTCTCCATTTGAACCATTT 2040
DB 1981 CACGAGCTTCCAGAAAAGCGTCCACATTTTCAGCACTCTGCTCTCCATTTGAACCATTT 2040
QY 2041 CGGAAAAAGCAACGATTTGAAGAAATTAAGGAGTCTGATTAAGAAATGAATATAGATG 2100
DB 2041 CGGAAAAAGCAACGATTTGAAGAAATTAAGGAGTCTGATTAAGAAATGAATATAGATG 2100
QY 2101 CTGGCCAGCTTTTCATTTAAGGAAATAGGAAGCATTAAGTAAATTTTAGTGTAGT 2160
DB 2101 CTGGCCAGCTTTTCATTTAAGGAAATAGGAAGCATTAAGTAAATTTTAGTGTAGT 2160
QY 2161 TTTTAAATAGTCTCTGTATTTATTTAGAAATGAACAGGAGGAGGAAACAAAG 2220
DB 2161 TTTTAAATAGTCTCTGTATTTATTTAGAAATGAACAGGAGGAGGAAACAAAG 2220
QY 2221 ATTCCCTTGAATTTAGATCAAAATTTAGTAAATTTGTTTATGCTGCTCTGATATAACAC 2280
DB 2221 ATTCCCTTGAATTTAGATCAAAATTTAGTAAATTTGTTTATGCTGCTCTGATATAACAC 2280
QY 2281 TTTCCAGCCTATAGCAGAGGACATTTTCAGAGTTCGAATATAGAGACTGTGTTCAATGTT 2340
DB 2281 TTTCCAGCCTATAGCAGAGGACATTTTCAGAGTTCGAATATAGAGACTGTGTTCAATGTT 2340

Db 2281 TTTCCAGCCTATAGCAGACACATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTCT 2340
QY 2341 AAAGACTGAGCAGAACTGAAAAATTTACTATTGGATATTCAATCTTTCTTTATATATGTC 2400
Db 2341 AAAGACTGAGCAGAACTGAAAAATTTACTATTGGATATTCAATCTTTCTTTATATATGTC 2400
QY 2401 ATTGTCAACAATTTAAATATATCTACCAAGTACAGAAATGTGGAAGAAAAACCG 2456
Db 2401 ATTGTCAACAATTTAAATATATCTACCAAGTACAGAAATGTGGAAGAAAAACCG 2456

RESULT 2
US-10-186-399-1
; Sequence 1, Application US/10186399
; Publication No. US20020173481A1
; GENERAL INFORMATION:
; APPLICANT: Ekman, Niklas
; APPLICANT: Arighi, Elena
; APPLICANT: Vastrik, Imre
; APPLICANT: Tamagnone, Luca
; APPLICANT: Allitalo, Kari
; TITLE OF INVENTION: REGULATION OF VASCULAR ENDOTHELIUM USING BMX TYROSINE
; TITLE OF INVENTION: KINASE
; FILE REFERENCE: 28113/31941A
; CURRENT APPLICATION NUMBER: US/10/186,399
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 08/320,432
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1:
; LENGTH: 2456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-186-399-1

Query Match 100.0%; Score 2456; DB 13; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAAGCAGGAAACAGCTGAGCGGATGATATATGGATACAAAAATCTATTCTAGAAAGAA 60

QY 61 CTTCCTCTCAAAAGATCAGCAAGAAAGAAATGTCCACCAATATTTACAAAGAACGG 120
Db 61 CTTCCTCTCAAAAGATCAGCAAGAAAGAAATGTCCACCAATATTTACAAAGAACGG 120

QY 121 CTTTCTTTGTTTACCACCAACAAACCTTTCCCTACTATGATATGACAAATGAAAGGGGC 180
Db 121 CTTTCTTTGTTTACCACCAACAAACCTTTCCCTACTATGATATGACAAATGAAAGGGGC 180

QY 181 AGCAGAAAAGGATCCATTGAAATTAAGAAATCAGATGTGAGAGAAATGAAATCTCGAG 240
Db 181 AGCAGAAAAGGATCCATTGAAATTAAGAAATCAGATGTGAGAGAAATGAAATCTCGAG 240

QY 241 GAGCAGACCCCTGTAGAGACAGTACCCATTCAGATTTGCTATTAAGAGATGGGCTTC 300
Db 241 GAGCAGACCCCTGTAGAGACAGTACCCATTCAGATTTGCTATTAAGAGATGGGCTTC 300

QY 301 TATGTCATATGATCAATTAAGAGACCGAGTACAGTGGTTGAAAGCATACAAAGAG 360
Db 301 TATGTCATATGATCAATTAAGAGACCGAGTACAGTGGTTGAAAGCATACAAAGAG 360

QY 361 ATAAGGGTAAACCCCACTGCTGCTCAAGTACCATAGTGGTTCTCTGTCAGCGGAG 420
Db 361 ATAAGGGTAAACCCCACTGCTGCTCAAGTACCATAGTGGTTCTCTGTCAGCGGAG 420

QY 421 TTCCCTGTGTGTCAGCAGCTGTAAAGCAGCCCGAGGATGTACCTCTGCGAAAGCATAT 480
Db 421 TTCCCTGTGTGTCAGCAGCTGTAAAGCAGCCCGAGGATGTACCTCTGCGAAAGCATAT 480

QY 481 GCTAATCTGCATCTGCACTCAATGAAGAGAAACACAGATTTCCACCTTCCACAGACA 540

Db 481 GCTAATCTGCATCTGCACTCAATGAAGAGAAACACAGATTTCCACCTTCCACAGACA 540
QY 541 GTGCTGAAGATACCTCGGGCAGTTCCTGTCTCAAAAATGGATGACACCATCTTCAAGTACC 600
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QY 601 ACTCTAGCCCAATATGACAAACGAAATCAAGAAAAAATATGGCTCCAGCCACCATCTTCA 660
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QY 721 TTCAACATGCACTATATCCAAAGGAGAGACTTCCCTGAGCTGGTGGCAAGTAAGAAACTG 780
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QY 781 AAAAGTAGCAGCAGCAGTGAAGATGTTCAAGCAGTAACCAAAAGAAAGAAATGTGAAT 840
Db 781 AAAAGTAGCAGCAGCAGTGAAGATGTTCAAGCAGTAACCAAAAGAAAGAAATGTGAAT 840

QY 841 CACACACCTCAAAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGAA 900
Db 841 CACACACCTCAAAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGAA 900

QY 901 AACCTGGATGATTATGACTGTTGTTGTTGAATCTCCAGATCAACAATCTGAACATTA 960
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QY 1081 CAGCTGCATACAAATGCTGAGAACAAATATATACCTGCGAAGAACTACTGTTTGTATTC 1140
Db 1081 CAGCTGCATACAAATGCTGAGAACAAATATATACCTGCGAAGAACTACTGTTTGTATTC 1140

QY 1141 ATTCCAAAGCTTATTCATTCATCAACACAATTCAGCAGGCATGATCACACGGCTCCG 1200
Db 1141 ATTCCAAAGCTTATTCATTCATCAACACAATTCAGCAGGCATGATCACACGGCTCCG 1200

QY 1201 CACCTGTCTCAACAAAGGCCAACAGTCCCGACTCTCTGTCCCTGGGAAATGGAAATC 1260
Db 1201 CACCTGTCTCAACAAAGGCCAACAGTCCCGACTCTCTGTCCCTGGGAAATGGAAATC 1260

QY 1261 TGGGAAGCTGAAAGAGAGAGATTAACCTTTGTTGAAGAGCTGGGAAGTGGCCAGTTTGA 1320
Db 1261 TGGGAAGCTGAAAGAGAGAGATTAACCTTTGTTGAAGAGCTGGGAAGTGGCCAGTTTGA 1320

QY 1321 GTGCTCCAGCTGGGCAAGTGAAGGGCAGTATGATGTTGCTGTTAAGATGATCAAGAG 1380
Db 1321 GTGCTCCAGCTGGGCAAGTGAAGGGCAGTATGATGTTGCTGTTAAGATGATCAAGAG 1380

QY 1381 GGCTCCATCATCAAGATGAATTTCTTTCAGGAGGCCAGACTATGATGAACCTCAGGCAT 1440
Db 1381 GGCTCCATCATCAAGATGAATTTCTTTCAGGAGGCCAGACTATGATGAACCTCAGGCAT 1440

QY 1441 CCCAAGCTGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTACT 1500
Db 1441 CCCAAGCTGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTACT 1500

QY 1501 GAATATATGAAGCAATGGCTGCTTGTGAATTAACCTGAGGAGTCAAGGAAAGGACTTGAA 1560
Db 1501 GAATATATGAAGCAATGGCTGCTTGTGAATTAACCTGAGGAGTCAAGGAAAGGACTTGAA 1560

QY 1561 CTTTCCAGCTCTTAGAAATGTCTGAGAGATGTCTGTAAGGCATGGCTTCTTGGAGAGT 1620

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DB 901 AACCTGGATGATTATGACTGGTTGCTGTGTAACATCTCCAGATCAAAATCTGAACAGTTA 960
QY 961 CTCAGACAAAGGGAAGAGGAGCATTTATGTTAGAAATTCGAGCCCAAGTGGGAATG 1020
DB 961 CTCAGACAAAGGGAAGAGGAGCATTTATGTTAGAAATTCGAGCCCAAGTGGGAATG 1020
QY 1021 TACACAGTGTCTTATTTAGTAAAGGCTGTGAATGATATAAAGGAACTGTCAAAACATTTAC 1080
DB 1021 TACACAGTGTCTTATTTAGTAAAGGCTGTGAATGATATAAAGGAACTGTCAAAACATTTAC 1080
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DB 1081 CACGTGCATACAAATGCTGAGACAAATATACCTGGCAGAAACTACTGTTTGAATCC 1140
QY 1141 ATTCGAAGCTTATTCATATATCAACACAAATTCAGCAGGCATGATCACGGCTCCGC 1200
DB 1141 ATTCGAAGCTTATTCATATATCAACACAAATTCAGCAGGCATGATCACGGCTCCGC 1200
QY 1201 CACCTGTGTCAACAAAGGCGCAAGGTCCCGACTCTGTGCTCCCTGGGAAATGGAATC 1260
DB 1201 CACCTGTGTCAACAAAGGCGCAAGGTCCCGACTCTGTGCTCCCTGGGAAATGGAATC 1260
QY 1261 TGGAACTGAAAGAGAGAGATTAACCTTGTGGAAGGAGCTGGGAAGTGGCACTTTGGA 1320
DB 1261 TGGAACTGAAAGAGAGAGATTAACCTTGTGGAAGGAGCTGGGAAGTGGCACTTTGGA 1320
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DB 1321 GTGCTCAGCTGGCAAGTGAAGGGCAGTATGATGTTGCTGTTAAGATGATCAAGGAG 1380
QY 1381 GGCTCCATGTCAGAGATGAATCTTTCAGGAGCCCGAGATGATGAATCAAGCTCAGCCAT 1440
DB 1381 GGCTCCATGTCAGAGATGAATCTTTCAGGAGCCCGAGATGATGAATCAAGCTCAGCCAT 1440
QY 1441 CCCAAGCTGGTAAATCTATGAGTGTGTTCGAAAGGAATACCCCATATACATAGTAGT 1500
DB 1441 CCCAAGCTGGTAAATCTATGAGTGTGTTCGAAAGGAATACCCCATATACATAGTAGT 1500
QY 1501 GAATATATAGCAATGCTGCTGTGTAATACCTGAGGATGACGGAAGAGACTTCAA 1560
DB 1501 GAATATATAGCAATGCTGCTGTGTAATACCTGAGGATGACGGAAGAGACTTCAA 1560
QY 1561 CCTTCCAGCTCTTGAATGCTACGATGCTGTGAAGCATGGCCCTTCTTGAGAGT 1620
DB 1561 CCTTCCAGCTCTTGAATGCTACGATGCTGTGAAGCATGGCCCTTCTTGAGAGT 1620
QY 1621 CACCAATTCATACACCGGACTTGGCTGCTGTAACCTGCTGGGACAGAGATCTCTGT 1680
DB 1621 CACCAATTCATACACCGGACTTGGCTGCTGTAACCTGCTGGGACAGAGATCTCTGT 1680
QY 1681 GTGAAAGTATCTGACTTTGGAATGACAGGATGTTCTTGTATGACCACTATGTCAGTTCA 1740
DB 1681 GTGAAAGTATCTGACTTTGGAATGACAGGATGTTCTTGTATGACCACTATGTCAGTTCA 1740
QY 1741 GTCGGAACAAAGTTTCCAGTCAAGTGTGCTCAGCTCCAGAGGTTGTTTCATTTCAATATAC 1800
DB 1741 GTCGGAACAAAGTTTCCAGTCAAGTGTGCTCAGCTCCAGAGGTTGTTTCATTTCAATATAC 1800
QY 1801 AGCAGCAAGTCAGACGCTATGGGCAATTTGGGATGCTGTGTTGGAGGTTTCCAGCTGGGG 1860
DB 1801 AGCAGCAAGTCAGACGCTATGGGCAATTTGGGATGCTGTGTTGGAGGTTTCCAGCTGGGG 1860
QY 1861 AAGCAGCCCTATGACTTTGATGACAACTCCAGGTGTTCTCAAGGTTCTCCAGGGCCAC 1920
DB 1861 AAGCAGCCCTATGACTTTGATGACAACTCCAGGTGTTCTCAAGGTTCTCCAGGGCCAC 1920
QY 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCAATCTACCAAGATCATGATCAGCTGCTGG 1980
DB 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCAATCTACCAAGATCATGATCAGCTGCTGG 1980
QY 1981 CACGAGCTTCCAGAAAGCGTCCACATTTTCAGCAACTCTCTTCCATTTGAACCACTT 2040

DB 1981 CACGAGCTTCCAGAAAGCGTCCACATTTTCAGCAACTCTCTTCCATTTGAACCACTT 2040
QY 2041 CGGGAAGAGCAAGCATTTGAAGAGAAATTTAGGAGTCTGTGATAAGAAATGATATAGATG 2100
DB 2041 CGGGAAGAGCAAGCATTTGAAGAGAAATTTAGGAGTCTGTGATAAGAAATGATATAGATG 2100
QY 2101 CTGGCCAGCATTTTCATTTAAGGAAAGTGAAGGCAATTAATTTTAGCTAGT 2160
DB 2101 CTGGCCAGCATTTTCATTTAAGGAAAGTGAAGGCAATTAATTTTAGCTAGT 2160
QY 2161 TTTTAATAGTGTCTCTGTATTTAGTATTTAGAAATGACAAAGGCAAGGAAACAAAG 2220
DB 2161 TTTTAATAGTGTCTCTGTATTTAGTATTTAGAAATGACAAAGGCAAGGAAACAAAG 2220
QY 2221 ATTCCTTTCAATTTAGTCAATTTAGTAAATTTTGTGTTTATGCTGCTGATATACAC 2280
DB 2221 ATTCCTTTCAATTTAGTCAATTTAGTAAATTTTGTGTTTATGCTGCTGATATACAC 2280
QY 2281 TTTCCAGCTATAGCAGAGCAGCATTTTCAGACTGCAATATAGAGACTGTGTTTATGCTG 2340
DB 2281 TTTCCAGCTATAGCAGAGCAGCATTTTCAGACTGCAATATAGAGACTGTGTTTATGCTG 2340
QY 2341 AAAGACTGAGCAGAACTGAAATTTACTTTATTTGGATATTCATTTCTTTTATATGTC 2400
DB 2341 AAAGACTGAGCAGAACTGAAATTTACTTTATTTGGATATTCATTTCTTTTATATGTC 2400
QY 2401 ATTTGTCACAACTTTAAATATATACTACCAAGTACAGAAATGTCGAAA 2446
DB 2401 ATTTGTCACAACTTTAAATATATACTACCAAGTACAGAAATGTCGAAA 2446

RESULT 4

US-10-171-581-317
; Sequence 317, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 317
; LENGTH: 2604
; TYPE: DNA
; ORGANISM: Homo sapiens.
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF045459
; DATABASE ENTRY DATE: 2001-06-18
US-10-171-581-317

Query Match 97.9%; Score 2404.2; DB 14; Length 2604;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2422; Conservative 0; Mismatches 8; Indels 3; Gaps 1;
QY 21 GACGATGATAATATGGATACAAATCTATTCTAGAGAACTTCTTCTCAAAAGATCACA 80
DB 175 GAAAGATGATAATATGGATACAAATCTATTCTAGAGAACTTCTTCTCAAAAGATCACA 234
QY 81 GCAAAAGAGAAATGTCCACCAATTAATTTACAAAGAACGGCTTTTGTGTTTGACCAAAAC 140
DB 235 GCAAAAGAGAAATGTCCACCAATTAATTTACAAAGAACGGCTTTTGTGTTTGACCAAAAC 294
QY 141 AAACCTTTCTACTATGATATGACAAATGAAAGGGGACGAGGAAAGGATCCATTGA 200
DB 295 AAACCTTTCTACTATGATATGACAAATGAAAGGGGACGAGGAAAGGATCCATTGA 354
QY 201 AATTAAGAAATCAGATGCTGGAGAACTAAATCTCGAGGAGCAGACGCTGTAGAGAG 260

355	Db	 AATTAAGAAATTCAGATGTTGGAGAAAGTAAATCTCGAGGAGCAGCGCTGTAGAGAG	414
261	QY	 ACAGTACCATTTCAGATTGCTATAAAGATGGGCTTCTATGTCTATGCATCAAAATGA	320
415	Db	 ACAGTACCATTTCAGATTGCTATAAAGATGGCTTCTCTATGTCTATGCATCAAAATGA	474
321	QY	 AGAGAGCCGAAGTCAGTGGTTGAAAGCATTTACAAAAGAGATPAAAGGGTAAACCCACCT	380
475	Db	 AGAGAGCCGAAGTCAGTGGTTGAAAGCATTTACAAAAGAGATPAAAGGGTAAACCCACCT	534
381	QY	 GCTGGTCAAGTACCATAGTGGGTTCTTCGTGGACGGGAAGTCTCTGTGTGGCCAGAGAG	440
535	Db	 GCTGGTCAAGTACCATAGTGGGTTCTTCGTGGACGGGAAGTCTCTGTGTGGCCAGAGAG	594
441	QY	 CTGTAAAGCAGCCCCAGGATGTACCTCTCTGGGAAGCATATGCTAAATCTGCATACTGCAGT	500
595	Db	 CTGTAAAGCAGCCCCAGGATGTACCTCTCTGGGAAGCATATGCTAAATCTGCATACTGCAGT	654
501	QY	 CAATGAAGAGAAACACAGAGTTCGCCACTTCCACAGACAGAGTCTGCTGAAGATATCGGGC	560
655	Db	 CAATGAAGAGAAACACAGAGTTCGCCACTTCCACAGACAGAGTCTGCTGAAGATATCGGGC	714
561	QY	 AGTTCCTGTCTCAAAATGATGCACCATCTTCAAGTACCACCTCTAGCCCAATATGACAA	620
715	Db	 AGTTCCTGTCTCAAAATGATGCACCATCTTCAAGTACCACCTCTAGCCCAATATGACAA	774
621	QY	 CGAATCAAGAAATAACTATGGCTCCAGCCACCATCTTCAAGTACCACCTCTAGCCCAAT	680
775	Db	 CGAATCAAGAAATAACTATGGCTCCAGCCACCATCTTCAAGTACCACCTCTAGCCCAAT	834
681	QY	 TGACAGCACTCAAGAAATCTATGGCTCCAGCCCAACTTCAAGTACCACCTCTAGCCCAAT	740
835	Db	 TGACAGCACTCAAGAAATCTATGGCTCCAGCCCAACTTCAAGTACCACCTCTAGCCCAAT	894
741	QY	 AAGGGAAGACTTCCCTGACTGGTGGGAAGTAAAGAAACTGAAAAGTATGACGACGAGTGA	800
895	Db	 AAGGGAAGACTTCCCTGACTGGTGGGAAGTAAAGAAACTGAAAAGTATGACGACGAGTGA	954
801	QY	 AGATGTTGCAAGCAGTAACCAAAAAGAAAGAAATGTGAATCACACCACCTCAAGATTTTC	860
955	Db	 AGATGTTGCAAGCAGTAACCAAAAAGAAAGAAATGTGAATCACACCACCTCAAGATTTTC	1014
861	QY	 ATGGGAATTCCTTGAGTCAAGTTCATCTGAAGAGAGGAAACCTGGATGATTATGACTG	920
1015	Db	 ATGGGAATTCCTTGAGTCAAGTTCATCTGAAGAGAGGAAACCTGGATGATTATGACTG	1074
921	QY	 GTATTGCTGTAACATCTCCAGATCACAACTGTAACAGTACTCAGACAAAGGGAAGA	980
1075	Db	 GTATTGCTGTAACATCTCCAGATCACAACTGTAACAGTACTCAGACAAAGGGAAGA	1134
981	QY	 AGGAGCATTTATGGTTAGAAATTCGAGCCAAAGTGGGAATGTACACAGTGTCTTATTAG	1040
1135	Db	 AGGAGCATTTATGGTTAGAAATTCGAGCCAAAGTGGGAATGTACACAGTGTCTTATTAG	1194
1041	QY	 TAAGGCTGTGAATGATAAAAAAGGAAGTGTCAAAACATTTACACGTGCATACAAATGCTGA	1100
1195	Db	 TAAGGCTGTGAATGATAAAAAAGGAAGTGTCAAAACATTTACACGTGCATACAAATGCTGA	1254
1101	QY	 GAACAAATTTATAGTGGCAGAAAATCTACTGTTTGTATTCCATTCCAAAGCTTATTCATTA	1160
1255	Db	 GAACAAATTTATAGTGGCAGAAAATCTACTGTTTGTATTCCATTCCAAAGCTTATTCATTA	1314
1161	QY	 TCATCAACAAATTCAGCAGGCATGATCACAGGCCTCCGCCACCTGTGTCAACAAGGC	1220
1315	Db	 TCATCAACAAATTCAGCAGGCATGATCACAGGCCTCCGCCACCTGTGTCAACAAGGC	1371
1221	QY	 CAACAAGTCCCGACTCTGTGTCCTGGGAAATGGAATCTGGGAAGTCAAAAAGAGAAGA	1280
1372	Db	 CAACAAGTCCCGACTCTGTGTCCTGGGAAATGGAATCTGGGAAGTCAAAAAGAGAAGA	1431
1281	QY	 GATTACCTTTGAAGGAGCTGGGAAGTGGCCAGTTTGGAGTGGTCCAGCTGGGCAAGTG	1340

QY 2421 TACTACCAAGTACAGAAATCTGGAAAAA 2453
 Db 2572 TACTACCAAGTACAGAAATCTGGAAAAA 2604

RESULT 5

US-09-977-269-3
 ; Sequence 3, Application US/09977269
 ; Patent No. US20020082037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ULLRICH, AXEL
 ; APPLICANT: GISHIZKY, MIKHAIL
 ; APPLICANT: SURES, IRVINGARD
 ; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 ; FILE REFERENCE: 038602/1260
 ; CURRENT APPLICATION NUMBER: US/09/977,269
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 08/232,545
 ; PRIOR FILING DATE: 1994-04-22
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 2500
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (82)..(2106)
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
 ; OTHER INFORMATION: kinase 2
 ; US-09-977-269-3

Query Match 97.6%; Score 2397.6; DB 9; Length 2500;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 2417; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 22 ACGGATGATATATGGATACAAATCTATTCTAGAAAGCTTCTTCAAAAGATACAG 81
 Db 70 AAGGATGATATATGGATACAAATCTATTCTAGAAAGCTTCTTCAAAAGATACAG 129
 QY 82 CAAAAGAGAAATGTCCACCAATTAATACAAAGAGCGCTTTTGTGACCAAAACA 141
 Db 130 CAAAAGAGAAATGTCCACCAATTAATACAAAGAGCGCTTTTGTGACCAAAACA 189
 QY 142 AACCTTTCTCTATGATATGACAAATGAAAGAGGCGCAGCAAAAGGATCCATTGAA 201
 Db 190 AACCTTTCTCTATGATATGACAAATGAAAGAGGCGCAGCAAAAGGATCCATTGAA 249
 QY 202 ATTAAGAAATCAGATGTGGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA 261
 Db 250 ATTAAGAAATCAGATGTGGAGAAAGTAAATCTCGAGGAGCAGACGCTGTAGAGAGA 309
 QY 262 CAGTACCCATTTCAGATGTCTATAAGATGGCTTCTCTATGCTATGATCATCAATGAA 321
 Db 310 CAGTACCCATTTCAGATGTCTATAAGATGGCTTCTCTATGCTATGATCATCAATGAA 369
 QY 322 GAGAGCGGAAGTCAAGTGGTGAAGCATTTACAAAGAGATTAAGGGTAAACCCCACTG 381
 Db 370 GAGAGCGGAAGTCAAGTGGTGAAGCATTTACAAAGAGATTAAGGGTAAACCCCACTG 429
 QY 382 CTGGTCAAGTACCATAGTGGTGTCTTCGTGGAGGGAAGTTCCTGTGTTGCCAGCAGGC 441
 Db 430 CTGGTCAAGTACCATAGTGGTGTCTTCGTGGAGGGAAGTTCCTGTGTTGCCAGCAGGC 489
 QY 442 TGTAAGCACCACCCAGGATGATACCTCTGGAGAGCATATGCTAATCTGCATACGATG 501
 Db 490 TGTAAGCACCACCCAGGATGATACCTCTGGAGAGCATATGCTAATCTGCATACGATG 549
 QY 502 AATGAAGAGAAACACAGAGTTCACCTCTCCAGAGAGTGTGTAAGATACCTCGGGCA 561
 Db 550 AATGAAGAGAAACACAGAGTTCACCTCTCCAGAGAGTGTGTAAGATACCTCGGGCA 609

QY 562 GTTCTCTGTTCTCAAAATGGATGACCAATCTTCAAGTACCACCTCTAGCCCAATATGACAAC 621
 Db 610 GTTCTCTGTTCTCAAAATGGATGACCAATCTTCAAGTACCACCTCTAGCCCAATATGACAAC 669
 QY 622 GAATCAAGAGAAACTATGGCTCCAGCACCACATCTTCAAGTACCAGTCTAGCGCAATAT 681
 Db 670 GAATCAAGAGAAACTATGGCTCCAGCACCACATCTTCAAGTACCAGTCTAGCGCAATAT 729
 QY 682 GACAGCAACTCAAGAGAAATCTATGGCTCCAGCACCACATCTTCAAGTACCAGTCTAGCGCAATAT 741
 Db 730 GACAGCAACTCAAGAGAAATCTATGGCTCCAGCACCACATCTTCAAGTACCAGTCTAGCGCAATAT 789
 QY 742 AGGAGAGACTTCCCTGACTGGTGGCAAGTAAGAGAAACTGAAAGTACAGCAGCAGTGA 801
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 QY 802 GATGTTGCAAGCAGTAACCAAAAGAGAAATGTGAATACACACACCTTCAAGATTTTCA 861
 Db 850 GATGTTGCAAGCAGTAACCAAAAGAGAGAAATGTGAATACACACACCTTCAAGATTTTCA 909
 QY 862 TGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAGAAACCTGGATGATTATGACTGG 921
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 Db 1150 AACAAATTTATACCTGGCAGAGAACTACTGTTTGTGATTCATTCCTCAAGCTTATTCATAT 1209
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 Db 1210 CATCAACAAATTCAGCAGGATGATCACAGGCTCCGCGACCTGTGTCAACAAGGCC 1269
 QY 1222 AACAGGTCCCGACTCTGTCTCCCTGGGAAATGGAATCTGGGAACTGGAAGAGAGAGAG 1281
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 QY 1282 ATTTACCTTTGAGAGGAGCTGGGAAAGTGGCAGTGGAGTGGTCCAGCTGGGCAAGTGG 1341
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 QY 1342 AAGGGCAGATGATGTTGCTGTTAAGATGATCAAGAGAGGCTCCATGTCAGAGATGAA 1401
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 QY 1402 TTCTTTTCAGGAGGCCAGACTATGATGAAACTCAGCCATCCCAAGCTGGTAAATTCAT 1461
 Db 1450 TTCTTTTCAGGAGGCCAGACTATGATGAAACTCAGCCATCCCAAGCTGGTAAATTCAT 1509
 QY 1462 GGAGTGTGTTCAAAGGAATACCCCATATACATAGTACTGATATATATAGCAATGGCTGC 1521
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Db 130 CAAAGAAGAAATGTCAACCAATATATACAAAGAGCGCTTTTGTGTTTACCAAAACA 189
-QY 142 AACCTTCCCTACTATGATATGACAAATGAAAGAGGCGCAGCAAGAGATCCATTGAA 201
Db 190 AACCTTCCCTACTATGATATGACAAATGAAAGAGGCGCAGCAAGAGATCCATTGAA 249
QY 202 ATTAAGAAAATCAGATGTGTGGAGAAAGTAAATCTCAGAGGAGCAGAGCCCTGTAGAGAGA 261
Db 250 ATTAAGAAAATCAGATGTGTGGAGAAAGTAAATCTCAGAGGAGCAGAGCCCTGTAGAGAGA 309
QY 262 CAGTACCATTTCAGATGTCTATAAGATGGGCTTCTCTATGTCTATGATCAATCAATGAA 321
Db 310 CAGTACCATTTCAGATGTCTATAAGATGGGCTTCTCTATGTCTATGATCAATCAATGAA 369
QY 322 GAGAGCGAGTCACTAGTGTGAAGCAATACAAAAGAGATTAAGGGGTAAACCCCACTG 381
Db 370 GAGAGCGAGTCACTAGTGTGAAGCAATACAAAAGAGATTAAGGGGTAAACCCCACTG 429
QY 382 CTGGTCAAGTACCATAGTGGGTTCTCGTGACGGGAAGTTCCTGTGTGTCAGCAGAGC 441
Db 430 CTGGTCAAGTACCATAGTGGGTTCTCGTGACGGGAAGTTCCTGTGTGTCAGCAGAGC 489
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Db 1210 CATCAACAAATTCAGCAGGCATGATCACAGGCTCCGCGACCCCTGTGTCAACAAGGCC 1269

QY 1222 AACAGGTCCCGACTCTGTGTCCCTGGGAAATGGAATCTGGGAACTGAAAAGAGAGAG 1281
Db 1270 AACAGGTCCCGACTCTGTGTCCCTGGGAAATGGAATCTGGGAACTGAAAAGAGAGAG 1329
QY 1282 ATTACCTTGTGTTAAAGGAGCTGGGAAAGTGGCCAGTTTGGAGTGGTCCAGCTGGGCAAGTGG 1341
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QY 1342 AAGGGCAGTATGATGTGCTGTTAAGATGATCAAGGAGGCTCCATGTCAGAAAGTGA 1401
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QY 1402 TTCTTTTCAAGGAGGCCAGACTATGATGAAACTCAGCCATCCCAAGCTGGTTAAATTCAT 1461
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QY 1762 AAGTGGTCAGCTCCAGAGTGTCTTCAATTAACATACAGCAGCAAGTCAGACGTATGG 1821
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QY 1822 GCATTTGGGATTCCTGATGTGGAGGTGTTCAGCCCTGGGAAAGCAGCCCTATGACTTGTAT 1881
Db 1870 GCATTTGGGATTCCTGATGTGGAGGTGTTCAGCCCTGGGAAAGCAGCCCTATGACTTGTAT 1929
QY 1882 GACAACTCCAGCTGGTCTGAAAGTCTCCAGGSCCAGAGCTTTACGGCCCCCAGCTG 1941
Db 1930 GACAACTCCAGCTGGTCTGAAAGTCTCCAGGSCCAGAGCTTTACGGCCCCCAGCTG 1989
QY 1942 GCATCGGACACCATCTACAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAGCT 2001
Db 1990 GCATCGGACACCATCTACAGATCATGTACAGCTGCTGGCAGCAGCTTCCAGAAAGCT 2049
QY 2002 CCCACATTTCAAGCAACTCTCTCTTCCATTTGAACACTTTCGGGAAAAGCAGCAATGGA 2061
Db 2050 CCCACATTTCAAGCAACTCTCTCTTCCATTTGAACACTTTCGGGAAAAGCAGCAATGGA 2109
QY 2062 AGAAGAAATAGGAGTCTGATAGAATGAATATAGATGCTGGCCAGCAATTTTCATTCAT 2121
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Db 2290 AATTAGTAATTTTGTGTTTATGCTGCTGTATATAACACTTTCAGGCTTATAGCAGAGC 2348

Db 1781 AATACACAGCTCAGTAGGCTCAATTTCCAGTCCGGTGGTCCCGACCGAGTCTCTGA 1840
QY 1787 ATTACTTCAATACAGCAGCAAGTACAGAGTATGGGATTTGGGATCTCTGTATGGGAGG 1846
Db 1841 TGTATAGCAAGTTCAGCAGCAATCTGACATTTGGGCTTTTGGGGTTTGTATGTGGGAAA 1900
QY 1847 TGTTCAGCTGGGAGCAGCCCTATGACTTTATGACAACTCCCGAGTGGTTCGTAAGG 1906
Db 1901 TTTACTCCCTGGGAGAGTGGCATATGAGAGATTTACTAACAGTGAGACTGCTGAACACA 1960
QY 1907 TCTCCAGGCGCCACAGGCTTTACCGGCCCCACCTGGCATCGGACACCATCTACCAGATCA 1966
Db 1961 TTGCCCAAGGCTACGCTCTACAGGCTCTCTGCTTCAGAGAGGTATATACCATCA 2020
QY 1967 TGTACAGTGTGGCAGCAGCTTCCAGAAAGCGTCCCAATTTTACGCAACTCTCTGTCT 2026
Db 2021 TGTACAGTGTGGCAGCAGCTTCCAGAAAGCAGATGAGCGTCCCACTTTCAAAAATTTCTCTGAGCA 2080
QY 2027 COATTGAACCACTTCGGGAAAAGA 2051
Db 2081 ATATTCTAGATGCTCATGGATGAAGA 2105

RESULT 11
US-10-220-801-4
; Sequence 4, Application US/10220801
; Publication No. US20030125235A1
; GENERAL INFORMATION:
; APPLICANT: FOXWELL, Brian Maurice John
; TITLE OF INVENTION: TREATMENT OF DISEASES ASSOCIATED WITH CYTOKINE PRODUCTION WITH
; TITLE OF INVENTION: INHIBITORS OF THE TEC FAMILY OF PROTEIN TYROSINE KINASES
; FILE REFERENCE: 117-412 / N83427B JP
; CURRENT APPLICATION NUMBER: US/10/220,801
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: PCT/GB01/00949
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: GB 0005345.4
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: MS Word
; SEQ ID NO 4
; LENGTH: 2582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-801-4

Query Match
Best Local Similarity 19.6%; Score 480.2; DB 14; Length 2582;
Matches 737; Conservative 0; Mismatches 428; Indels 0; Gaps 0;

QY 887 CTGAAGAAGAGAAACCTGGATGATTTATGACTGGTTCGTGTAACATCTCCAGATCAC 946
Db 972 CTGAAGCAGAGACTCCATAGAAATGTATGAGTGTATTCCTCAACACATGACTCGGAGTC 1031
QY 947 AATCTGAACAGTACTACAGAAAGGAAAGAGAGCAATTTATGTTAGAAATTCGA 1006
Db 1032 AGGCTGACCAACTGCTAAGCAAGAGGGAAGAGAGGTTTCATTGTCAGAGACTCCA 1091
QY 1007 GCCAAGTGGGAATGTACACAGTGTCTTATTTAGTAGGCTGTGATGATGATAAAGGAA 1066
Db 1092 CCAAGCTGGCAATATACAGTGTCTGTGTTTCTAAATTCACAGGGGACCTCCAGGGG 1151
QY 1067 CTGTCAACATATACACGTGTACATAAATGTGTGAGAACAAATTTATACCTGGCAGAAAACT 1126
Db 1152 TGATACGTCATATGTTGTGTCTCCACACCTCAGAGCCAGTATTACCTGGCTGAGAGC 1211
QY 1127 ACTGTTTGTATCCATTCGAAGCTTATTCATTAATCAACAAATTCAGCAGCATCA 1186
Db 1212 ACCTTTTTCAGCAGCCTCCCTGAGCTCATTAATCACTACATCAGCAGCAACTCTGAGGACTCA 1271
QY 1187 TCACAGGCTCCGCGCCACTGTGTCAACAAGAGGCAAGAGTCCCGACTCTGTGTCC 1246

Db 1272 TATCCAGGCTCAATATCCAGTCTCTCAACAAAACAGAAATGACACCTTCCACTGCAGGCC 1331
QY 1247 TGGGAAATGGAATCTGGGAACTGAAAGAGAGAGATTAACCTTGTGTTGAAGAGCTGGAA 1306
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QY 1307 GTGGCCAGTTTGGAGTGGTCCAGCTGGGCAAGTGGAGAGGGCCAGTATGATGTTGCTGTTA 1366
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QY 1367 AGATGATCAAGAGGCTCCATCTCAGAGATCAATTTCTTTCAGGAGGCCAGACTATGA 1426
Db 1452 AGATGATCAAGAGGCTCCATCTCTGAAGATCAATTTCTTTCAGGAGGCCAGACTATGA 1511
QY 1427 TGAATCTCAGCAGCTCCCAAGCTGGTTAAATTTCTATGGAGTGTGTTTCAAGAAATACCCCA 1486
Db 1512 TGAATCTTCCCATGAGAGCTGGTGCAGTTGTATGGCGTCTGCACCAAGCAGCGCCCA 1571
QY 1487 TATACATAGTACTGAATATATAAGCAATGGCTGCTTGTGTAATTAACCTGAGGAGTCAG 1546
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QY 1607 CCTCTTGGAGAGTACCAATTCATACCCGGGACTTGGCTGCTGCTGCTGCTGCTGCTGCTG 1666
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QY 1667 ACAGAGATCTCTGTGTAAGTATCTGACTTTGGAAATGACAAGATGATGTTCTTGTATGACC 1726
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Db 1872 TGTATAGCAAGTTCAGCAGCAATCTGACATTTGGGCTTTTGGGTTTTCATGTTGGGAAA 1931
QY 1847 TGTTCAGCTGGGAGAGCAGCCCTATGACTTTGATGACAACTCCCGAGTGGTCTGAGG 1906
Db 1932 TTTACTCCCTGGGAGAGATGCCATATGAGAGATTTACTAACAGTGAAGTCTGCTGAACACA 1991
QY 1907 TCTCCAGGCGCACAGGCTTTACCGGCCCCACCTGCGCATCGGACACCATCTACCAGATCA 1966
Db 1992 TTGCCCAAGGCTACGCTCTTACAGGCTCTATCGGCTTCAGAGAAAGGTATATACCATCA 2051
QY 1967 TGTACAGCTGCTGGCAGCAGCTTCCAGAAAGCGTCCCGACATTTTCAGCAACTCTGCTGCTT 2026
Db 2052 TGTACAGTGTGTTGTTTGAAGAGCAGATGAGCGTCCCGACTTTTCAAAATTTCTCTGAGCA 2111
QY 2027 COATTGAACCACTTCGGGAAAAGA 2051
Db 2112 ATATTCTAGATGCTCATGGATGAAGA 2136

RESULT 12
US-09-735-103-2
; Sequence 2, Application US/09735103
; Patent No. US20010005589A1
; GENERAL INFORMATION:
; APPLICANT: Mano, Hiroyuki
; APPLICANT: Sakata, Tsunekaki
; APPLICANT: Hasegawa, Mamoru
; TITLE OF INVENTION: Promoter
; FILE REFERENCE: 50026/011002
; CURRENT APPLICATION NUMBER: US/09/735,103
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/142,529
; PRIOR FILING DATE: 1998-09-09

;; PRIOR APPLICATION NUMBER: PCT/JP97/00741
;; PRIOR FILING DATE: 1997-03-10
;; PRIOR APPLICATION NUMBER: JP 8/54294
;; PRIOR FILING DATE: 1996-03-12
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 2574
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-735-103-2

Query Match 17.9%; Score 439.4; DB 9; Length 2574;
Best Local Similarity 61.5%; Pred. No. 3.6e-107;
Matches 723; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

QY 899 AAAACCTGGATATACACCTGTTTCTGCTGTAACATCTCAGATCACAATCTGAACAGT 958
DB 830 ACAACTTAGATCAATATAGTGGTACTGCGAGAAATACCAAGAGCAAGCAAGCAGC 889
QY 959 TACTCAGACAAAGAGGAAAGAGGAGCATTTATGTTTGTAGAAATTCAGAGCCAAAGTGGAA 1018
DB 890 TCCTCAGACGAGAGATTAAGAGAGGTGTTTATGTTGAGAGACTCCAGTCAACAGGCT 949
QY 1019 TGTACACAGTGTCTCTATTTAGTAAAGCTGTGAATGATAAAAAAGAACTCTCAAAACAT 1078
DB 950 TGTACACTGTCTCCCTTTACACAAAGTTTGGGGGAGAGGCTCATCAGTTTTCAGGCATT 1009
QY 1079 ACCAGCTGCA-----TACAAATGCTGAGACAAATATATACCTGGCAGAAAACACTACTGTT 1132
DB 1010 ATCACAATAAGGAAACAGCAACATCCCAAGAGAGTATATACCTGGCAGAGAGCATGCTT 1069
QY 1133 TTGATTCATCCCAAGCTTATTCATATATCAACACAAATTCAGCAGGCGATGATCACAC 1192
DB 1070 TCGGGTCCATCCCTGAGATCATTAATCAACAGCAATATCGCGAGGGCTGTGCACCA 1129
QY 1193 GGCTCCGCCACCTGTGTCAACAAAGGCCAAAGGTCGCCGACTCTGTGTCCCTGGGAA 1252
DB 1130 GGCTGGCGTACCCGCTAGTACAAAGGGGAGAGAGCTGCCACTACTCCGSCCTTCAGCT 1189
QY 1253 ATGCAATCTGGAACTGAAAGAGAGAGATTAACCTTTGTAAGGAGCTGGGAGTGGCC 1312
DB 1190 ATGATAAGTGGGAGATTAAACCATCAGAGCTGAGCTTTATGAGAGAGTTGGGGAGCGGAC 1249
QY 1313 AGTTTGGAGTGTCCAGCTGGCAGTGGAGGGGCGAGTATGTTGCTCTTAAAGTGA 1372
DB 1250 TGTTTGAGTGTGAGGCTGGCAGTGGCGGGCCAGTCAAAAGTGGCCATCAAGCTA 1309
QY 1373 TCAAGGAGGGCTCCATGTCAAGAGATGAATTTCTTCAGGAGGGCCAGACTATGATGAAC 1432
DB 1310 TCCGGGAAGGGCCATGTGTCAAGAGGATTTTCATAGAGAGCTAAAGTCATGATGAAGC 1369
QY 1433 TCAGCCATCCCAAGCTGTTAAATTCATAGAGTGTGTTCAAGAAATACCCCATATACA 1492
DB 1370 TGACACACCCCAAGCTGTGACAGCTCTATGTTGTATGACCCAGCAGAGGCCATCTACA 1429
QY 1493 TAGTACTGATATATAGCAATGGCTGTCTGCTGAATTAATCACTGAGGAGTCAAGGAAAG 1552
DB 1430 TCGTTACCGAGTTTCATGAAGCGGGCTGCCCTCTCAATTTCTCCGCGAGAGACAAGGCC 1489
QY 1553 GACTTGAACCTTCCAGCTCTTGAATATGCTGCTAGATGCTGTGAAGGATGGCCTTCT 1612
DB 1490 ATTTACAGCAGACATGCTGTGAAGCATGTGTCAGATGCTGTGAAGGATGAGATACC 1549
QY 1613 TGGAGAGTCAACATTCATACACCGGACTTGGCTGTCTGTAACCTGTTGTTGTCAGACAG 1672
DB 1550 TGGAGAGAACTTCTTCATCCACAGAGACCTGGCTGCCAGAAATGCTACTGATGAAG 1609
QY 1673 ATCTCTGTGAAAGTATCTGACATTTGGAATGACAAGGATATGTTCTGTATCAGCAGATG 1732
DB 1610 CAGGAGTTGTCAAAAGTATCTGATTTTGGAAATGGCCAGGTACGTTCTGTGATCAGTACA 1669
QY 1733 TCAGTTTCAGTGGGAACAAAGTTTCCAGTCAAGTGGTCCAGTCCAGAGGTGTTTCTACT 1792

RESULT 13
US-10-045-428A-2
;; Sequence 2, Application US/10045428A
;; Publication No. US20020115845A1
;; GENERAL INFORMATION:
;; APPLICANT: Mano, Hiroyuki
;; APPLICANT: Sakata, Tsuneaki
;; APPLICANT: Hasegawa, Mamoru
;; APPLICANT: Tabata, Toshiaki
;; TITLE OF INVENTION: Promoter
;; FILE REFERENCE: 50026/011003
;; CURRENT APPLICATION NUMBER: US/10/045,428A
;; PRIORITY FILING DATE: 2002-04-15
;; PRIOR APPLICATION NUMBER: 09/735,103
;; PRIOR FILING DATE: 2000-12-12
;; PRIOR APPLICATION NUMBER: 09/142,529
;; PRIOR FILING DATE: 1999-08-12
;; PRIOR APPLICATION NUMBER: PCT/JP97/00741
;; PRIOR FILING DATE: 1997-03-10
;; PRIOR APPLICATION NUMBER: JP 8/54294
;; PRIOR FILING DATE: 1996-03-12
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 2574
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-045-428A-2

Query Match 17.9%; Score 439.4; DB 13; Length 2574;
Best Local Similarity 61.5%; Pred. No. 3.6e-107;
Matches 723; Conservative 0; Mismatches 446; Indels 6; Gaps 1;
QY 899 AAAACCTGGATATACACCTGTTTCTGCTGTAACATCTCAGATCACAATCTGAACAGT 958
DB 830 ACAACTTAGATCAATATAGTGGTACTGCGAGAAATACCAAGAGCAAGCAAGCAGC 889
QY 959 TACTCAGACAAAGGAAAGAGGAGCATTTATGTTTGTAGAAATTCGAGCCAAAGTGGAA 1018
DB 890 TCCTCAGAACGAGATTAAGAGAGGTGTTTATGTTGAGAGACTCCAGTCAACAGGCT 949
QY 1019 TGTACACAGTGTCTCTATTTAGTAAAGCTGTGAATGATAAAAAAGAACTGTCAAAACAT 1078
DB 950 TGTACACTGTCTCCCTTTACACAAAGTTTGGGGGAGAGGCTCATCAGGTTTTCAGGCATT 1009
QY 1079 ACCAGCTGCA-----TACAAATGCTGAGACAAATATATACCTGGCAGAAAACACTACTGTT 1132
DB 1010 ATCACAATAAGGAAACAGCAACATCCCAAGAGAGTATTTACCTGGCAGAGAGCATGCTT 1069

QY	1133	TTGATTCCATTCCAAAGCTTATTTCAATATCATCAACACAATTCAGCAGGCGATGATCACAC	11192
Db	1070	TCGGGTCCATCTCTGAGATCATTTGAATATCACAAAGCACATTCGGCAGGCTTGTCAACA	11129
QY	1193	GGCTCCGGCACCCCTGTGTCAACAAGAGCCCAACAAAGTCCCGGACTCTGTGTCCCTGGAA	1252
Db	1130	GGCTGGGGTACCCGGGTACAGTACAAAGGGGAAGAACGCTCCCACTACTGGCGGCTTCAGCT	11189
QY	1253	ATGGAATCTCGGAACTCAAAAGAGAAGATTAACCTTTGTGAAGGAGCTGGGAAGTGGCC	13112
Db	1190	ATGATAAGTGGAGATTAAACCATCAGAGCTGACCTTTATGAGAGAGTTGGGAGCGGAC	1249
QY	1313	AGTTTGGAGTGTCCAGCTCGGCAAGTGGGAAGGGGCGAGTATGATGTTCGTGTAAAGTGA	1372
Db	1250	TGTTTTGGAGTGTGTGAGCTTTGGCAAGTGGCGGGCCAGTACAAAGTGGCCATCAAAAGCTA	1309
QY	1373	TCAAGGAGGCGCTCCATCTCGAAGAGATGAATTCCTTCAGGAGGCCAGACATCATCAAAAC	1432
Db	1310	TCGGGANGCGCATGTGTGAAGAGATTTCTATAGGGAAGCTAAAGTCATGATGAAGC	1369
QY	1433	TCAGCCATCCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAAGGAATACCCCATATACA	1492
Db	1370	TGACACACCCCAAGCTGGTACAGCTCTATGGTGTATGCACCCAGCAGAGCCCATCTACA	1429
QY	1493	TAGTGACTGAATATATAAGCAATGGCTGTCTGCTGAATTACTTGAGGATCGACGGAAG	1552
Db	1430	TCGTTTACCGAGTTCATGTGAACGGGGGTGCCCTTCTGAATTTCTCCGGCAGAGACAAGCC	1489
QY	1553	GACTTGAACCTTCCCAGCTCTTAGAATGTGTACGATGTCTGTGAAGGATCGCCCTTCT	1612
Db	1490	ATTTACGACAGACATGCTGCTGAAGCATGTGTCAAGATGTCTGTGAAGGGATGGAGTACC	1549
QY	1613	TGGAGAGTCAACCAATTCATACACGGGACCTTGGCTGCTCTAACTGCTTGGTGGACAGAG	1672
Db	1550	TGGAGAGAACTTCTTCATCCACAGAGACCTGGCTGCCAGAAATGTCTAGTGAATGAAG	1609
QY	1673	ATCTCTGTGTGAAGATATCTGACTTTTGGGAATGACAAAGGTATGTTCGTGATGACCAATG	1732
Db	1610	CAGGAGTTTGTCAAGTATCTGATTTTGGAAATGGCCAGGTACGTTCTGGATGATCATACA	1669
QY	1733	TCAGTTTCAGTCGGNACAAACATTTCCAGTCAAGTGGTCAGCTCCAGAGGTGCTTTCACTACT	1792
Db	1670	CAAGTTCTTCTTGGCCCAAGTTCCTCTGTGAAGTGGTGTCCCCAGAAAGTGTTTAATTACA	1729
QY	1793	TCAAATACAGCAGCAAGTCAAGATATGGGCATTTGGGATTCCTGATGTGGGAGGTGTCA	1852
Db	1730	GCCGCTTTAGCAGCAAGTCAAGAGCTGTGTGTCTGTTTGGTGTGCTAATGTGGGAAATATCA	1789
QY	1853	GCCTGGGGAAGCAGCCCTATGACTTTGATGACAACCTCCAGGTGGTGTCTGAAAGGTCTCCC	1912
Db	1790	CAGAAGGACGAGTATGCCCTTTTGAAGAACAACCAATTTACGAAGTGGTAAACATGGTGACTC	1849
QY	1913	AGGGCCACAGCGTTTACCGGCCCCACCTGCGCATCGGACACCATCTACACAGATCATGTACA	1972
Db	1850	GTGGCCACCCTCCACCGGCCCAAGCTGCTGCTTCCAAATATTTGTATGAGGTGATGCTGA	1909
QY	1973	GCTGCTGGCAGAGCTTCCAGAAAGAGCGTCCCAATTTTCAGCAACTCTCTCTTCCATTG	2032
Db	1910	GATGCTGGCAAGAGAGACCAAGAGGAGGCGCTTCTTGTGAAGACTTCTCTCCGTACCATAG	1969
QY	2033	AACCATTCTCGGGAAGAGACAGCATTTGAAGAAGA	2067
Db	1970	ATGAACATAGTTGAATGTGAAGAACTTTTCGAAGA	2004

RESULT 14

RESULT 14
IIS-09-919-172-84

: Sequence 84, Application US/09919172

; Patent No. US20020119463A1

; GENERAL INFORMATION;

APPLICANT: Faris, Mary

APPLICANT: Turner, Christopher M.

; TITLE OF INVENTION: PROSTATE CANCER MARKERS

```
Db      1626  CGGAGCTTGTAAAGTATCTGATTTTGAATGGCCAGGTATGTCTGGATGATCAGTACA 1685
Qy      1733  TCAGTTTCAGTCGGAACAAAGCTTTCCAGTCAAGTGGTCAGCTCCAGAGGTCTTTTCATTACT 1792
Db      1686  CAAATTCTCTGTGTAGTTTCCCTGTGTAAGTGGTGTCCACCTGAAGTGTTTAAATTACA 1745
Qy      1793  TCAATACAGCAAGTCAAGCTATGGGCATTTGGGATCCCTGATGTGGAGGTGTTC 1852
Db      1746  GCGCTTCAGCAGCAATCAGATGTCTGGTCAATTTGGTGTTTAAATGTGGAAGTATCA 1805
Qy      1853  GCGTGGGAGCAGCCCTATGACTTGTATGACAACCTCCAGGTGGTGTCTGAAAGTCTCCC 1912
Db      1806  CGGAAGGCGAAGTCCCTTTTGAATAATACACCAATATGAAGTGGTAAACCATGGTACTC 1865
Qy      1913  AGGCGCACAGGCTTTACCGGCCACCTGGCATCGGCAGCACCATCTACCAGATCATGTACA 1972
Db      1866  GAGGCCACGACTCTACCGCCGAAAGTGGCGTCCCAACTATGTATGAGGTGATGCTGA 1925
Qy      1973  GCTGCTGGCAGCAGCTTCCAGAAAAGCGTCCACATTTACAGCACTCTCTGCTTCCATTG 2032
Db      1926  GATGTTGGCAGGAGAACAGAGGAGGCGCTTCTTTCGAAGATCTGCTCGGCACATAG 1985
Qy      2033  AACCACTTCGGGAAAAGAACAGCATTTGAAGAAGAAATTAGAGTG 2078
Db      1986  ATGAACCTAGTTGAATGTGAAGAACTTTTGAAGATAAGTGATGTG 2031
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RESULT 15

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US-10-220-801-6
; Sequence 6, Application US/10220801
; Publication No. US20030125235A1
; GENERAL INFORMATION:
; APPLICANT: FOXWELL, Brian Maurice John
; TITLE OF INVENTION: TREATMENT OF DISEASES ASSOCIATED WITH CYTOKINE PRODUCTION WITH
; TITLE OF INVENTION: INHIBITORS OF THE TEC FAMILY OF PROTEIN TYROSINE KINASES
; FILE REFERENCE: 117-412 / N85427B JP
; CURRENT APPLICATION NUMBER: US/10/220,801
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: PCT/GB01/00949
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: GB 0005345.4
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: MS Word
; SEQ ID NO 6
; LENGTH: 3593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-801-6
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Query Match      15.88; Score 388; DB 14; Length 3593;
Best Local Similarity 59.6%; Pred. No. 2.9e-93;
Matches 674; Conservative 0; Mismatches 450; Indels 6; Gaps 1;

Qy      899  AAAACCTGGATGATTGACTGTTTCTGCTGTAACATCTCCAGATCAACAATCTGAACAGT 958
Db      775  ACACTTAGATCAATATGATGTTTGCAGAAATATGAATAGAACGAGCAGAGCAAC 834
Qy      959  TACTCAGACAAAAGGAAAAAGAGGACATTTATGGTTAGAAATTCAGGCCAAGTGGGAA 1018
Db      835  TCCTCCGACGTGAAGATAAAGAGGTGGTTTATGGTAAGGATTCAGTCAGCAACAGGCT 894
Qy      1019  TGTACACAGTCTCTTATTTAGTAAGCTGTGAATGATATAAAGGAACATGTCAAACT 1078
Db      895  TGTACACAGTCTCCCTTTATACCAAGTTTGGAGGAGAGGTTTCATCGGGTTTATAGGCA 954
Qy      1079  ACCACGTGCA-----TACAAATGCTGAGAACAAATATACCTGGCAGAAAACTACTGTT 1132
Db      955  ATCATATAAGAAACAAACAAACATCTCCAAGAGAGTATACCTAGCTGAAAAACATGCTT 1014
Qy      1133  TTGATTCATTCCAAAGCTTTATTCATTATCATCAACAATTCAGCAGGATGATCACAC 1192
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Search completed: August 20, 2003, 18:35:56
Job time : 562 secs

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Db      1015  TTGECTCCATTCTGTAGATTATTGAATATATCAATAGCACATGTCAGCAGGACTTGTCACCA 1074
Qy      1193  GGTCTCCGCCACCTGTGTCAACAAAGGCCAACAAAGTCCCGACTCTGTGTCTCCCTGGGAA 1252
Db      1075  GGCTTCGGTACCCAGTTAGTCTGAAGGGAGAGTGCACCCACCACCTGTCAGGATTCAGCT 1134
Qy      1253  ATGGAATCTGGGAACCTGAAAGAGAGAGATTACCTTGTGTAAGAGCTGGGAAGTGGCC 1312
Db      1135  ATGAGAATGGGAGATTAAACCTTTCAGAACTGACCTTTATGAGGAAATTTGGGAAGTGGAC 1194
Qy      1313  AGTTTGAGTGGTCCAGCTGGCAAGTGGAGGGGACGATGATGTCTGCTGTTAAGATGA 1372
Db      1195  TGTGTGAGTGGTGGAGCTTGGCAATGGCGAGCCCAACAAAGTCCCAATCAAAAGCTA 1254
Qy      1373  TCAAGGAGGGCTCCATGTCAGAAATGAATTTCTTTCAGGAGGCCAGACATATGATGAAC 1432
Db      1255  TTCGGGAAGTGCATGTGCGAGGAGGACTTTATAGAGAAGCTAAAGTGTGATGAAC 1314
Qy      1433  TCAGCCATCCCAAGCTGGTTAAATTCATGAGGTGTGTTCAAGGAATACCCCATATACA 1492
Db      1315  TGACACACCCGAAAGTTAGTGCAGCTTTATGGTGTGTCACCCAGCAGAGCAACATATACA 1374
Qy      1493  TAGTGACTGAATATATGAAGCAATGCTGCTGCTGAATTACTGAGGAGTCACGGAAG 1552
Db      1375  TTGTTACTGATTCATGAAAGGGGCTGCTCTCAATTTCTCCGACAGACAAAGTCT 1434
Qy      1553  GACTTGAACCTTCCAGCTCTTAGAAATGTCTAGATGTCTGTAAGGATGTCGCTTCT 1612
Db      1435  ATTTCACTAGACAGCTACTGCTGAGCATGCTCAGGATGTGTGGAAGGGATGGAGTATC 1494
Qy      1613  TGGAGAGTCACCAATTCATACACCGGACCTTGGCTGCTGCTGTAACCTTGTGTTGGACAGAG 1672
Db      1495  TGGAGACAAACAGCTTCATCCACAGAGATCTGGCTGCCAGAAAATTTGTCTAGTAAGTGAGG 1554
Qy      1673  ATCTCTGTGAAAAGTATCTGACTTTGGAATGCAAGTATGTTCTTGTATGACCAAGTATG 1732
Db      1555  CGGAGTGTGAAAAAGTATCTGATTTGGAATGGCAGGATGTTCTGATGATCATCAGTACA 1614
Qy      1733  TCAGTTTCAGTCGGGAACAAAGTTTCCAGTCAAGTGTGTCAGCTCCAGAGTGTGTTCACT 1792
Db      1615  CAAGTTCTCTGTTGGTGAAGTTTCTGTGAAGTGGTGTCCACCTGAAGTGTGTTAATTACA 1674
Qy      1793  TCAATATACAGCAGCAAGTCAGACGATATGGGCAATTTGGGATCCTGATGTGGGAGGTGTTCA 1852
Db      1675  GCCGCTTCAGCAGCAAAATCAGATGCTGCTGTCATTTGGTGTGTTTAAATGTGGGAAGTATCA 1734
Qy      1853  GCCTGGGAAGCAGCCCTATGACTGTGATGACAACCTCCAGGTGGTCTTGAAGGTCTCCC 1912
Db      1735  CGGAAGGCAGAAATGCTTTTGAATAATACACCAATTTATGAAGTGGTAAACCATGGTACTC 1794
Qy      1913  AGGCCCACAGGCTTTACGGCCCCACCTGGCATCGGACACCATCTACCAGATCATGTACA 1972
Db      1795  GAGGCCACCGACTCTACCAGCCGAAAGTGGCGTCCCAACTATGTGTATGAGGTGATGCTGA 1854
Qy      1973  GCTCTGCTGACGAGGCTTCCAGAAAAGCGTCCACATTTTCAGCAACTCTCTG 2022
Db      1855  GATCTTGGCAGGAGAAACCCAGGGAAGGCGCTTCTTTCGAAGATCTGCTG 1904
```


PR 29-MAR-2000; 2000US-0538445.
PR 07-OCT-1994; 94US-0320432.

PA (EKMA//) EKMAN N.
PA (ARIG//) ARIGHI E.
PA (VAST//) VASTRIK I.
PA (TAMA//) TAMAGNONE L.
PA (ALIT//) ALITALO K.

PI Ekman N, Arighi E, Vastrik I, Tamagnone L, Alitalo K;

DR WPI; 2003-352595/33.
DR P-PSDB; ABU08376.

Treating or preventing arteriosclerosis, e.g. arteriosclerosis, in a patient comprises regulating Bmx tyrosine kinase activity in endocardial and arterial endothelial cells to regulate growth signals in vascular endothelia -

PS Example 1; Page 9-10; 23pp; English.

The present invention relates to regulation of vascular endothelium using bone marrow tyrosine kinase gene in chromosome X (Bmx TK). The invention discloses a method for treating arteriosclerosis in a patient by regulating Bmx tyrosine kinase activity in endothelial and arterial endothelial cells to regulate growth signals in endothelium or adjacent smooth muscle, to regulate the inflammatory response, or to improve the non-thrombogenic properties of vascular endothelium. The method of the invention and tyrosine kinase inhibitors are useful for preventing or treating arteriosclerosis, or narrowing of the lumen of an artery of the heart, e.g. arteriosclerosis. The method is also useful for diagnosing a human disease associated with Bmx dysfunction, or for identifying agents that affect a Bmx tyrosine kinase signalling pathway. The present sequence encodes human Bmx TK. The gene encoding human Bmx TK maps to chromosome Xp22.2.

SQ Sequence 2456 BP; 805 A; 495 C; 549 G; 607 T; 0 other;

Query Match	100.0%	Score 2456;	DB 25;	Length 2456;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2456:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:

QY		1	GCAAGCAGGAAACAAGCTGAGACGGATGATTAATATGGATACAAAATCTATTCTAGAAGAA	60
Db		1	GCAAGCAGGAAACAAGCTGAGACGGATGATTAATATGGATACAAAATCTATTCTAGAAGAA	60
QY		61	CTTCTTCTCAAAAGATCACAGCAAAAGAGAAATGTCACCAATAATATTACAAAGACGG	120
Db		61	CTTCTTCTCAAAAGATCACAGCAAAAGAGAAATGTCACCAATAATATTACAAAGACGG	120
QY		121	CTTTTGTGTTTGACCAAAAACAACTTCCCTACTATGAATATGACAAAATCAAAAGGGGC	180
Db		121	CTTTTGTGTTTGACCAAAAACAACTTCCCTACTATGAATATGACAAAATGAAAGGGGC	180
QY		181	AGCAGAAAAGATCCATTGAAATTAAAGAAAATCAGATGTGGAGAAAGTAAATCTCGAG	240
Db		181	AGCAGAAAAGATCCATTGAAATTAAAGAAAATCAGATGTGGAGAAAGTAAATCTCGAG	240
QY		241	GAGCAGACGCGTGTAGAGAGACAGTACCATTTCAGATTGTCATATAAGATGGGCTTCTC	300
Db		241	GAGCAGACGCGTGTAGAGAGACAGTACCATTTCAGATTGTCATATAAGATGGGCTTCTC	300
QY		301	TATGTCTATGCATCAAAATCAACAGAGCGCAAGTCAGTGTCAAGAGCATTAACAAAAGAG	360
Db		301	TATGTCTATGCATCAAAATGAAGAGAGCGCAAGTCAGTGTGTTGAAAGCATTTACAAAAGAG	360
QY		361	ATAAGGGGTAAACCCACCTGCTGGTCAAGTACCATTAGTGGGTTCTTCGTGGACGGGAAG	420
Db		361	ATAAGGGGTAAACCCACCTGCTGGTCAAGTACCATTAGTGGGTTCTTCGTGGACGGGAAG	420
QY		421	TTCTCTGTGTGCCACGACAGCTGTAAAGCAGCCCCAGGATGTACCTCTGGGAAGCATAT	480

QY 301 TATGTCATCATCAATGAAGAGAGCCGAAGTCAGTGGTTGAAGCATTACAAAAGAG 360
DB 301 TATGTCATCATCAATGAAGAGAGCCGAAGTCAGTGGTTGAAGCATTACAAAAGAG 360
QY 361 ATAAGGGGTAAACCCCACTGCTGGTCAAGTACCATAGTGGTCTTCGTGGAGGGAAG 420
DB 361 ATAAGGGGTAAACCCCACTGCTGGTCAAGTACCATAGTGGTCTTCGTGGAGGGAAG 420
QY 421 TTCCTGTGTTGCAGAGAGCTGTAAAGCAGCCCGAGGATGTACCCCTCTGGGAGCATAT 480
DB 421 TTCCTGTGTTGCAGAGAGCTGTAAAGCAGCCCGAGGATGTACCCCTCTGGGAGCATAT 480
QY 481 GCTAACTGTCATCTGTCAGTCAATGAAGAGAGAGAGTTCCTCCAGCAGAGA 540
DB 481 GCTAACTGTCATCTGTCAGTCAATGAAGAGAGAGAGTTCCTCCAGCAGAGA 540
QY 541 GTGCTGAAGATACCTCGGGCAGTTCCTGTTCTCAAAATGGATGCACCATCTTCAAGTACC 600
DB 541 GTGCTGAAGATACCTCGGGCAGTTCCTGTTCTCAAAATGGATGCACCATCTTCAAGTACC 600
QY 601 ACTCTAGCCCAATATGACACGATCAAGAGAGAGAGTTCCTCCAGCAGAGAGTTCCTCA 660
DB 601 ACTCTAGCCCAATATGACACGATCAAGAGAGAGAGTTCCTCCAGCAGAGAGTTCCTCA 660
QY 661 AGTACAGTCTAGCGCAATATGACAGCACTCAAGAGAGAGTTCCTCCAGCAGAGAGTTCCT 720
DB 661 AGTACAGTCTAGCGCAATATGACAGCACTCAAGAGAGAGTTCCTCCAGCAGAGAGTTCCT 720
QY 721 TTCACATGTCAGTATATTCACGGAGAGACTTCCTGACTGGTGGCAAGTAAAGAGAGAGT 780
DB 721 TTCACATGTCAGTATATTCACGGAGAGACTTCCTGACTGGTGGCAAGTAAAGAGAGAGT 780
QY 781 AAAAGTAGCAGCAGTGAAGATGTTGCAAGCAGTAAACCAAGAGAGAGTAAAGAGAGAGT 840
DB 781 AAAAGTAGCAGCAGTGAAGATGTTGCAAGCAGTAAACCAAGAGAGAGTAAAGAGAGAGT 840
QY 841 CACACACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGAGT 900
DB 841 CACACACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGAGT 900
* QY 901 AACCTGATGATATGACTGGTGGTGGTAACTCTCCAGATCACAATCTGACAGTAA 960
DB 901 AACCTGATGATATGACTGGTGGTGGTAACTCTCCAGATCACAATCTGACAGTAA 960
QY 961 CTCAGACAAAGGAGAGAGAGCATTATGGTTAGAAATTCGAGCCCAAGTGGGAATG 1020
DB 961 CTCAGACAAAGGAGAGAGAGCATTATGGTTAGAAATTCGAGCCCAAGTGGGAATG 1020
QY 1021 TACACAGTGTCTTATTTAGTAAAGCTGTGAATGATAAAGAGAGTGTCAACATTTAC 1080
DB 1021 TACACAGTGTCTTATTTAGTAAAGCTGTGAATGATAAAGAGAGTGTCAACATTTAC 1080
QY 1081 CAGCTGATACAAATGCTGAGACAAATATACCTGGCAGAGAACTACTGTTTGTATTC 1140
DB 1081 CAGCTGATACAAATGCTGAGACAAATATACCTGGCAGAGAACTACTGTTTGTATTC 1140
QY 1141 ATTCGAAGCTTATTCATATCATCAACAAATTCAGCAGGATGATCAACGCTCCGC 1200
DB 1141 ATTCGAAGCTTATTCATATCATCAACAAATTCAGCAGGATGATCAACGCTCCGC 1200
QY 1201 CACCTGTGTCAACAAAGGAGAGTTCCTGTTGAAGAGCTGGGAGTGGCAGTGGGA 1260
DB 1201 CACCTGTGTCAACAAAGGAGAGTTCCTGTTGAAGAGCTGGGAGTGGCAGTGGGA 1260
QY 1261 TGGGAAGTGAAGAGAGAGTTCCTGTTGAAGAGCTGGGAGTGGCAGTGGGA 1320
DB 1261 TGGGAAGTGAAGAGAGAGTTCCTGTTGAAGAGCTGGGAGTGGCAGTGGGA 1320
QY 1321 GTGGTCCAGCTGGGAGTGGAGGGGAGTATGATGTTGCTGTAAAGATGATCAAGAG 1380
DB 1321 GTGGTCCAGCTGGGAGTGGAGGGGAGTATGATGTTGCTGTAAAGATGATCAAGAG 1380

QY 1381 GGTCTCATGTGAGAGATGAATTTCTTCAGGAGGCCAGACTATGATGAAACTCAGCCAT 1440
DB 1381 GGTCTCATGTGAGAGATGAATTTCTTCAGGAGGCCAGACTATGATGAAACTCAGCCAT 1440
QY 1441 CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTACT 1500
DB 1441 CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTACT 1500
QY 1501 GAATATATAAGCAATGCTGCTGCTGAATTTACCTGAGGAGTACGGAAAAAGGACTTCAA 1560
DB 1501 GAATATATAAGCAATGCTGCTGCTGCTGAATTTACCTGAGGAGTACGGAAAAAGGACTTCAA 1560
QY 1561 CCTTCCAGCTCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 CCTTCCAGCTCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 CACCAATTCATACACCGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 CACCAATTCATACACCGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 GTGAACTATCTGACTTTGGAATCACAAGGATGCTTCTTGATGACCACTATGTCAGTTCA 1740
DB 1681 GTGAACTATCTGACTTTGGAATCACAAGGATGCTTCTTGATGACCACTATGTCAGTTCA 1740
QY 1741 GTGGAACAAAGTTTCCAGTCAAGTGGTCACTCCAGAGTCTTTTCTTACTTCAATATAC 1800
DB 1741 GTGGAACAAAGTTTCCAGTCAAGTGGTCACTCCAGAGTCTTTTCTTACTTCAATATAC 1800
QY 1801 AGCAGCAAGTCAAGCTATGGCATTTGGGATCCTGATGTTGGAGGTTTTCAGCCTGGGG 1860
DB 1801 AGCAGCAAGTCAAGCTATGGCATTTGGGATCCTGATGTTGGAGGTTTTCAGCCTGGGG 1860
QY 1861 AAGCAGCCCTATGACTTTGATGACAACTCCAGCTGGTCTGGAAGTCTCCAGGCGCCAC 1920
DB 1861 AAGCAGCCCTATGACTTTGATGACAACTCCAGCTGGTCTGGAAGTCTCCAGGCGCCAC 1920
QY 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCACTTACAGATCATGTACAGCTGCTGG 1980
DB 1921 AGGCTTTACCGGCCCCACCTGGCATCGGACACCACTTACAGATCATGTACAGCTGCTGG 1980
QY 1981 CACGAGCTTCCAGAAAAGCGTCCCACTTTGAGCACTCCAGAGTCTCTGCTTCCATTTGA 2040
DB 1981 CACGAGCTTCCAGAAAAGCGTCCCACTTTGAGCACTCCAGAGTCTCTGCTTCCATTTGA 2040
QY 2041 CGGAAAAAGACACAGCATTTGAGAGAAATTTAGGAGTCTGATAGAAATGATATAGATG 2100
DB 2041 CGGAAAAAGACACAGCATTTGAGAGAAATTTAGGAGTCTGATAGAAATGATATAGATG 2100
QY 2101 CTGGCCAGCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
DB 2101 CTGGCCAGCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
QY 2161 TTTTAAATGATGTTCTGATGTTCTTATTTAGAAATGAAAGGAGGAGGAGGAGGAGGAG 2220
DB 2161 TTTTAAATGATGTTCTGATGTTCTTATTTAGAAATGAAAGGAGGAGGAGGAGGAGGAG 2220
QY 2221 ATTCCTTGAATTTAGATCAAAATAGTAAATTTTGTATGCTGCTCTGATATAGAAC 2280
DB 2221 ATTCCTTGAATTTAGATCAAAATAGTAAATTTTGTATGCTGCTCTGATATAGAAC 2280
QY 2281 TTTCCAGCTATAGCAGAGCAGATTTTACAGCTGCAATATAGAGACTGTGTCTATGCT 2340
DB 2281 TTTCCAGCTATAGCAGAGCAGATTTTACAGCTGCAATATAGAGACTGTGTCTATGCT 2340
QY 2341 AAAGACTGAGCAGAACTGAAAATTTACTTATTTGATATTTCTTCTTCTTCTTCTTCT 2400
DB 2341 AAAGACTGAGCAGAACTGAAAATTTACTTATTTGATATTTCTTCTTCTTCTTCTTCT 2400
QY 2401 ATTGTACACAAATTAATATATCTACCAAGTACAGAAATGTTGGAAGGAGGAGGAGGAG 2456
DB 2401 ATTGTACACAAATTAATATATCTACCAAGTACAGAAATGTTGGAAGGAGGAGGAGGAG 2456

1201 CACCCCTGTGTCAAAAGGCGCAAGAGTCCCGACTCTGTGTCTCTGGGAAATGGAATC 1260
 1201 CACCCCTGTGTCAAAAGGCGCAAGAGTCCCGACTCTGTGTCTCTGGGAAATGGAATC 1260
 1261 TGGGAAGTCAAAAGAGAGAGATTAACCTTGTGAAGAGAGTGGGAAGTGGCCAGTTTGGG 1320
 1261 TGGGAAGTCAAAAGAGAGAGATTAACCTTGTGAAGAGAGTGGGAAGTGGCCAGTTTGGG 1320
 1321 GTGGTCCAGCTGGGCAAGTGGAGGGGCGATGATGTTGCTGTTAAGATGATCAAGGAG 1380
 1321 GTGGTCCAGCTGGGCAAGTGGAGGGGCGATGATGTTGCTGTTAAGATGATCAAGGAG 1380
 1381 GGCTCATGTCAGAGATGAATTTCTTTCAGGAGGCGCAGACTATGATGAACATCAGCCAT 1440
 1381 GGCTCATGTCAGAGATGAATTTCTTTCAGGAGGCGCAGACTATGATGAACATCAGCCAT 1440
 1441 CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTGACT 1500
 1441 CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCATATACATAGTGACT 1500
 1501 GAATATAGCAATGGCTGCTGCTGAATTTACCTGAGAGTCAAGGAAAGAGCTGAA 1560
 1501 GAATATAGCAATGGCTGCTGCTGAATTTACCTGAGAGTCAAGGAAAGAGCTGAA 1560
 1561 CCTTCCAGCTCTTACAAATGTCTAGATGTCTGTGAAGGATGCGCTTCTTGGAGAGT 1620
 1561 CCTTCCAGCTCTTACAAATGTCTAGATGTCTGTGAAGGATGCGCTTCTTGGAGAGT 1620
 1621 CACCAATTCATACACGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 1621 CACCAATTCATACACGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 1681 GTGAAGTATCTGACATTTGGAATGACAAGATGTTCTGTGATGACCAAGTATGTCAGTTCA 1740
 1681 GTGAAGTATCTGACATTTGGAATGACAAGATGTTCTGTGATGACCAAGTATGTCAGTTCA 1740
 1741 GTCGGAACAAAGTTTCCAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 1741 GTCGGAACAAAGTTTCCAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 1801 AGCAGCAAGTCAAGATGATGGGATTTGGGATCCTGATGTGGAGGTGTTTCAGCCCTGGGG 1860
 1801 AGCAGCAAGTCAAGATGATGGGATTTGGGATCCTGATGTGGAGGTGTTTCAGCCCTGGGG 1860
 1861 AGCAGCCCTATGACATTTGATGACACTCCAGGTGCTGAGGTCTCCAGGCGCCAC 1920
 1861 AGCAGCCCTATGACATTTGATGACACTCCAGGTGCTGAGGTCTCCAGGCGCCAC 1920
 1921 AGGCTTTTACCGGCGCCACCTGGCATCGGACACCATCTACAGATCATGTACAGCTGCTGG 1980
 1921 AGGCTTTTACCGGCGCCACCTGGCATCGGACACCATCTACAGATCATGTACAGCTGCTGG 1980
 1981 CAGGAGCTTCCAGAAAGCGTCCACATTTACAGCAACTCCTGCTCTCCATTTGAACCACTT 2040
 1981 CAGGAGCTTCCAGAAAGCGTCCACATTTACAGCAACTCCTGCTCTCCATTTGAACCACTT 2040
 2041 CGGGAAGAGACAGCATTGAAGAGAAATAGGAGTGTGATGAAGAAATATAGATG 2100
 2041 CGGGAAGAGACAGCATTGAAGAGAAATAGGAGTGTGATGAAGAAATATAGATG 2100
 2101 CTGGCCAGCATTTTCATTTTAAAGAAAGTGAAGAGGAGTAAATTTTAAAGTAGT 2160
 2101 CTGGCCAGCATTTTCATTTTAAAGAAAGTGAAGAGGAGTAAATTTTAAAGTAGT 2160
 2161 TTTTAAATAGTGTCTCTGATGTTCTATTTATTTAGAAATGAACAGGAGGAAACAAAG 2220
 2161 TTTTAAATAGTGTCTCTGATGTTCTATTTATTTAGAAATGAACAGGAGGAAACAAAG 2220
 2221 ATTCCTTGAATTTAGATCAAAATAGTAAATTTTATGCTGCTCTGATATACAC 2280
 2221 ATTCCTTGAATTTAGATCAAAATAGTAAATTTTATGCTGCTCTGATATACAC 2280
 2281 TTTCCAGCTATAGCAGAGCAGCATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGT 2340

2281 TTTCCAGCTATAGCAGAGCAGCATTTTCAGACTGCAATATAGAGACTGTGTTTCATGTGT 2340
 2341 AAGACTGACAGCAACTGAAATTTACTTATTTGGATATTTCTTTCTTTATATTTGTC 2400
 2341 AAGACTGACAGCAACTGAAATTTACTTATTTGGATATTTCTTTCTTTATATTTGTC 2400
 2401 ATTGTCAACAATTAATATATACCAAGTACAGAAATGGAAGGAAAAAACCAG 2456
 2401 ATTGTCAACAATTAATATATATACCAAGTACAGAAATGGAAGGAAAAAACCAG 2456

RESULT 4
 AAS14050
 ID AAS14050 standard; cDNA; 2449 BP.
 XX
 AC AAS14050;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human cDNA encoding partial protein tyrosine kinase, Bmx.
 XX
 KW Immunosuppressive; antiinflammatory; osteopathic; antirheumatic;
 KW antiarthritic; dermatological; antipsoriatic; antiasthmatic; cytostatic;
 KW cardiant; antiarteriosclerotic; vasotropic; cerebroprotective;
 KW neuroprotective; nontropic; ophthalmological; immunosuppressive;
 KW hepatotropic; virucide; anti-HIV; immunomodulator; antithyroid; sepsis;
 KW septic shock; inflammation; crohn's disease; rheumatoid arthritis;
 KW leukopenia; osteoarthritis; spondyloarthropathy; psoriatic arthritis;
 KW severe steroid resistant asthma; pulmonary fibrosis; myocarditis;
 KW atherosclerosis; angina; vasculitis; reperfusion injury; infarction;
 KW stroke; multiple sclerosis; Alzheimer's disease; Graves ophthalmopathy;
 KW psoriasis; transplant rejection; acute alcoholic hepatitis; fibrosis;
 KW HIV; human immunodeficiency virus; cachexia; erythema nodosum lepromatum;
 KW borreliosis; meningococcal septicaemia; cancer; Human; Bmx; ss;
 KW antibacterial; protein tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..2061
 FT /*tag= a
 FT /product= "Bmx"
 FT /partial
 FT /note= "No start codon"
 XX
 PN WO200166107-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 06-MAR-2001; 2001WO-GB00949.
 XX
 PR 06-MAR-2000; 2000GB-0005345.
 XX
 PA (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
 XX
 PI Foxwell BMJ;
 XX
 DR WPI; 2001-602596/68.
 DR P-PSDB; AAU09013.
 XX
 PT Treating condition associated with cytokine production in a mammal,
 PT e.g. sepsis, septic shock, inflammation and Crohn's disease, comprises
 PT administering an inhibitor of a member(s) of the Tec family of protein
 PT tyrosine kinases
 XX
 PS Claim 23; Fig 18; 78pp; English.
 XX
 CC The invention relates to the use of inhibitors of the Tec family of
 CC protein tyrosine kinases to treat a condition associated with cytokine
 CC production in a mammal. The Tec family members are e.g. Bruton's
 CC tyrosine kinase (Btk), Tec, Itk, Txk or Bmx. The condition is especially
 CC sepsis, septic shock, inflammation, Crohn's disease or a condition

CC induced by TRR (Toll related receptor) ligand, LPS (lipopolysaccharide),
 CC zymosan or Gram-negative bacteria. The method may also be used for
 CC treating rheumatoid arthritis. Biological effects of LPS include fever,
 CC circulatory disturbances and vascular hypersensitivity to adrenergic
 CC drugs, leukopenia typically followed by leucocytosis, non-specific
 CC stimulation of B-lymphocytes to undergo blast transformation and
 CC proliferation, lethal toxicity and non-specific tolerance to endotoxin
 CC through repeated exposure to LPS. LPS also causes an increase in
 CC production of cytokines e.g. TNF. Conditions associated with IL-1beta
 CC and TNFalpha osteoarthritis, spondyloarthropathy, psoriatic arthritis,
 CC severe steroid resistant asthma, pulmonary fibrosis, myocarditis,
 CC atherosclerosis, angina with high CRP/IL-6, vasculitis, reperfusion
 CC injury, infarction, stroke, multiple sclerosis, Alzheimer's disease,
 CC Graves ophthalmopathy, psoriasis, transplant rejection, acute alcoholic
 CC hepatitis, fibrosis. Other conditions for which inhibitors of Tec
 CC family PTKs may be used include HIV (human immunodeficiency virus
 CC infection), cachexia, erythema nodosum lepromatum, borreliosis, or
 CC meningococcal septicemia, cancer, such as breast cancer, ovarian cancer
 CC or colon cancer. Many other examples of diseases are given in the
 CC specification. The present sequence encodes human Bmx.
 XX
 SQ Sequence 2449 BP; 797 A; 495 C; 548 G; 609 T; 0 other;

Query Match		98.7%;	Score 2424.4;	DB 22;	Length 2449;
Best Local Similarity		99.7%;	Pred. No. 0;		
Matches 2439;		Conservative	0;	Mismatches	6;
				Indels	1;
				Gaps	1;
QY	1	GCAGCAGGAGCAACAGCTGAGCGGATGATATATATGATGATACAAATCTATTCAGAGAA	60		
DB	1	GCAGCAGGAGCAACAGCTGAGCGGATGATATATATGATGATACAAATCTATTCAGAGAA	60		
QY	61	CTTCTTCTCAAAAGATCACAGCAAAAGAAAGAAATGTCCACCAATAATATACAAAGACGG	120		
DB	61	CTTCTTCTCAAAAGATCACAGCAAAAGAAAGAAATGTCCACCAATAATATACAAAGACGG	120		
QY	121	CTTTTGTGTTGACCAAAACAAACCTTTCTACTATGATGATGATGATGATGATGATGATG	180		
DB	121	CTTTTGTGTTGACCAAAACAAACCTTTCTACTATGATGATGATGATGATGATGATGATG	180		
QY	181	AGCAGAAAGATCCATGAAATTAAGAAATACAGATGATGATGATGATGATGATGATGATG	240		
DB	181	AGCAGAAAGATCCATGAAATTAAGAAATACAGATGATGATGATGATGATGATGATGATG	240		
QY	241	GAGCAGAGCCCTGTAGAGAGACAGTACCCATTTCAGATTGCTATTAAGAGTGGGCTTCTC	300		
DB	241	GAGCAGAGCCCTGTAGAGAGACAGTACCCATTTCAGATTGCTATTAAGAGTGGGCTTCTC	300		
QY	301	TATGCTATGATCAATTAAGAGAGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT	360		
DB	301	TATGCTATGATCAATTAAGAGAGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT	360		
QY	361	ATAAGGGTAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420		
DB	361	ATAAGGGTAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420		
QY	421	TTCCTGTGTTGCCAGCAGCTGTAAGACGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	480		
DB	421	TTCCTGTGTTGCCAGCAGCTGTAAGACGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	480		
QY	481	GCTAATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540		
DB	481	GCTAATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540		
QY	541	GTGCTGAAGATACCTCGGGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600		
DB	541	GTGCTGAAGATACCTCGGGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600		
QY	601	ACTTAGCCCAATATGCAAGCAATCAAGAAAGAAAGTATGGTCCCGACCACTCTTCA	660		
DB	601	ACTTAGCCCAATATGCAAGCAATCAAGAAAGAAAGTATGGTCCCGACCACTCTTCA	660		
QY	661	AGTACCAGTCTAGCGCAATATGACAGCAACTCAAGAAATCTATGGTCCCGACCAAC	720		
DB					

DB	661	AGTACCAGTCTAGCGCAATATGACAGCAACTCAAGAAATCTATGGCTCCCGACCAAC	720		
QY	721	TTCAACATGAGTATATTCACAGGAGAGTCTCCCTGACTGGTGGCAAGTAAGAAACTG	780		
DB	721	TTCAACATGAGTATATTCACAGGAGAGTCTCCCTGACTGGTGGCAAGTAAGAAACTG	780		
QY	781	AAAAGTAGCAGCAGCAGTGAAGATGTTGCAAGCAGTAACCCAAAGAAAGAAATGTCAT	840		
DB	781	AAAAGTAGCAGCAGCAGTGAAGATGTTGCAAGCAGTAACCCAAAGAAAGAAATGTCAT	840		
QY	841	CACACCACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAA	900		
DB	841	CACACCACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAGAGGAA	900		
QY	901	AACCTGGATGATATGACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	960		
DB	901	AACCTGGATGATATGACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	960		
QY	961	CTCAGACAAAAGGAAAAGAGGAGCATTTATGGTTAGAAATTCGAGCCCAAGTGGGAATG	1020		
DB	961	CTCAGACAAAAGGAAAAGAGGAGCATTTATGGTTAGAAATTCGAGCCCAAGTGGGAATG	1020		
QY	1021	TACACAGTCTCCTTATTTAGTAAAGCTGTGAATGATAAAAAGAACTGTCAACATAC	1080		
DB	1021	TACACAGTCTCCTTATTTAGTAAAGCTGTGAATGATAAAAAGAACTGTCAACATAC	1080		
QY	1081	CACGTGCATACAAATGCTGAGAACAAATATACCTGGCAGAAACTACTCTTTTGTATTC	1140		
DB	1081	CACGTGCATACAAATGCTGAGAACAAATATACCTGGCAGAAACTACTCTTTTGTATTC	1140		
QY	1141	ATTCCAAAGCTTATTCATTCATCAACAAATTCAGCAGGATGATCAGCAGCTCCGC	1200		
DB	1141	ATTCCAAAGCTTATTCATTCATCAACAAATTCAGCAGGATGATCAGCAGCTCCGC	1200		
QY	1201	CACCTGTGTCAACAAAGCCCAACAAAGTCCCGAGTCTGTGCTCCCTGGAAATGGAATC	1260		
DB	1201	CACCTGTGTCAACAAAGCCCAACAAAGTCCCGAGTCTGTGCTCCCTGGAAATGGAATC	1260		
QY	1261	TGGGAATCAAAAGAGAGATTAACCTTGTGGAAGAGCTGGGAAGTGGCCAGTTTGA	1320		
DB	1261	TGGGAATCAAAAGAGAGATTAACCTTGTGGAAGAGCTGGGAAGTGGCCAGTTTGA	1320		
QY	1321	GTGGTCCAGCTGGGCAAGTGAAGGGGAGTATGATGTTGCTGTTAAGATGATCAAGAG	1380		
DB	1321	GTGGTCCAGCTGGGCAAGTGAAGGGGAGTATGATGTTGCTGTTAAGATGATCAAGAG	1380		
QY	1381	GGCTCCATGTCAGAAAGATGAATTTCTTCAGGAGGCCAGACTATGATGAACCTCAGCAT	1440		
DB	1381	GGCTCCATGTCAGAAAGATGAATTTCTTCAGGAGGCCAGACTATGATGAACCTCAGCAT	1440		
QY	1441	CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGAGATACCCCATATACATAGTACT	1500		
DB	1441	CCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGAGATACCCCATATACATAGTACT	1500		
QY	1501	GAATATATGAAGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1560		
DB	1501	GAATATATGAAGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1560		
QY	1561	CCCTCCAGCTCTTAGAAATGTGCTACGATGCTGTGAAGGAGTGCCTTCTTGGAGAGT	1620		
DB	1561	CCCTCCAGCTCTTAGAAATGTGCTACGATGCTGTGAAGGAGTGCCTTCTTGGAGAGT	1620		
QY	1621	CACCAATTCATACACCGGACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1680		
DB	1621	CACCAATTCATACACCGGACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1680		
QY	1681	GTGAAGATATGACTTTGGAATGACAAAGTATGTTCTTGATGACCAAGTATGTCAGTTCA	1740		
DB	1681	GTGAAGATATGACTTTGGAATGACAAAGTATGTTCTTGATGACCAAGTATGTCAGTTCA	1740		
QY	1741	GTGGAACAAAGTTTCCAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800		
DB	1741	GTGGAACAAAGTTTCCAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800		

1801 AGCAGCAAGTCAGACGATGGGATTTGGATCTCTGATGTGGAGGTGTTCCAGCTGGG 1860
 1801 AGCAGCAAGTCAGACGATGGGATTTGGATCTCTGATGTGGAGGTGTTCCAGCTGGG 1860
 1861 AAGCAGCCCTATGACCTTGTATGACAACTCCAGGTGTTCTGAAAGGTCTCCAGGGCCAC 1920
 1861 AAGCAGCCCTATGACCTTGTATGACAACTCCAGGTGTTCTGAAAGGTCTCCAGGGCCAC 1920
 1921 AGCCTTACCGGCCCCACCTGGGATCGGACACCACTTACCAGATCATGATGCTGCTGG 1980
 1921 AGCCTTACCGGCCCCACCTGGGATCGGACACCACTTACCAGATCATGATGCTGCTGG 1980
 1981 CAGCAGCTTCCAGAAAGCGTCCACATTTTCAGCAACTCTCTGCTTCCATTGAACCACTT 2040
 1981 CAGCAGCTTCCAGAAAGCGTCCACATTTTCAGCAACTCTCTGCTTCCATTGAACCACTT 2040
 2041 CGGGAAGAACAGCAAGCAATTTGAAGAAATTTAGGAGTCTGATGAAGATGAATATAGATG 2100
 2041 CGGGAAGAACAGCAAGCAATTTGAAGAAATTTAGGAGTCTGATGAAGATGAATATAGATG 2100
 2101 CTGGCCAGCAATTTTCATCTATTTTAAGAAATTTAGGAGTCTGATGAAGATGAATATAGATG 2160
 2101 CTGGCCAGCAATTTTCATCTATTTTAAGAAATTTAGGAGTCTGATGAAGATGAATATAGATG 2160
 2161 TTTTAATAGTGTCTCTGATTTGCTATTTTGAAGATGAAGCAAGCAAGCAAGCAAGCAAG 2220
 2161 TTTTAATAGTGTCTCTGATTTGCTATTTTGAAGATGAAGCAAGCAAGCAAGCAAGCAAG 2220
 2221 ATTCCCTTGAATTTAGATCAAAATAGTAAATTTTGTATGCTGCTCTGATATACAC 2280
 2221 ATTCCCTTGAATTTAGATCAAAATAGTAAATTTTGTATGCTGCTCTGATATACAC 2279
 2281 TTTCCAGCTTATAGCAGACACATTTTCAGACTGCAATATAGAGACTGTGTTATGCTG 2340
 2280 TTTCCAGCTTATAGCAGACACATTTTCAGACTGCAATATAGAGACTGTGTTATGCTG 2339
 2341 AAAGACTGAGCAGCAACTGAAATAATTTACTTATTTGATATTTCTTTTCTTTATATGTC 2400
 2340 AAAGACTGAGCAGCAACTGAAATAATTTACTTATTTGATATTTCTTTTCTTTATATGTC 2399
 2401 ATTGTCAACAATTAATATATCTACCAAGTACAGAAATGTGAAA 2446
 2400 ATTGTCAACAATTAATATATCTACCAAGTACAGAAATGTGAAA 2445

RESULT 5

AAT00617 standard; cdna; 2494 BP.
 AC AAT00617;
 XX 26-MAR-1996 (first entry)
 XX Megakaryocyte kinase MKK2 cdna.
 XX Megakaryocyte kinase-2; MKK2; cytoplasmic tyrosine kinase;
 KW cellular signal transduction; leukaemia; myelofibrosis;
 KW gene therapy; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 PH CDS 76..2103
 FT /*tag= a
 FT
 XX W09529185-A1.
 XX 02-NOV-1995.
 XX 24-APR-1995; 95MO-US05008.
 XX 21-APR-1995; 95US-0426509.

22-APR-1994; 94US-0232545.
 (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 (SUGE-) SUGEN INC.
 Gishizky M, Sures I, Ullrich A;
 WPI; 1995-382959/49.
 P-PSDB; AAR84182.
 New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) -
 used to develop prods. for the treatment and diagnosis of kinase
 related signal transduction abnormalities.
 Claim 4; Fig 2A-B; 82pp; English.
 Overlapping cDNA clones were combined to obtain a sequence (AAT00617)
 coding for human megakaryocyte kinase MKK2 (AAR84182). The clones
 were isolated from a fetal brain library using degenerate primers
 CC (AAT00614-15) based on conserved regions within the kinase domain of
 CC receptor tyrosine kinases. MKK polynucleotides can be used in the
 CC prodn. in host cells of recombinant MKK, and in the gene therapy of
 CC diseases such as acute megakaryocytic leukaemia, myelofibrosis and
 CC acute megakaryocytic myelosis.
 XX Sequence 2494 BP; 797 A; 504 C; 553 G; 640 T; 0 other;
 SQ
 Query Match 97.3%; Score 2388.6; DB 16; Length 2494;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 2405; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 Qy 19 GAGACGGATGATATATGATACAAAATCTATTCTAGAAAGTCTTCTCTCAAAAGATCA 78
 Db 61 GAGTAGGATGATATATGATACAAAATCTATTCTAGAAAGTCTTCTCTCAAAAGATCA 120
 Qy 79 CAGCAAAAGAAAGAAATGTCACCAAAATTAATACAAAGAACGGCTTTTGTGACCAAA 138
 Db 121 CAGCAAAAGAAAGAAATGTCACCAAAATTAATACAAAGAACGGCTTTTGTGACCAAA 180
 Qy 139 ACAACCTTTCTACTACTGATATACAAAATTAATACAAAGAACGGCTTTTGTGACCAAA 198
 Db 181 ACAACCTTTCTACTACTGATATACAAAATTAATACAAAGAACGGCTTTTGTGACCAAA 240
 Qy 199 GAAATTAAGAAATCAGATGTGTGAGAAAGTAAATCTCGAGAGCAGACGCTGTAGAG 258
 Db 241 GAAATTAAGAAATCAGATGTGTGAGAAAGTAAATCTCGAGAGCAGACGCTGTAGAG 300
 Qy 259 AGACAGTACCCATTTTCAGATTTCTATAAAGATGGCTTCTCTATGCTATCATCAAT 318
 Db 301 AGACAGTACCCATTTTCAGATTTCTATAAAGATGGCTTCTCTATGCTATCATCAAT 360
 Qy 319 GAAGAGAGCCGAGTCACTGTTGAAGCATTACAAAAGAGATAGGGTTAAGGCTTACCCAC 378
 Db 361 GAAGAGAGCCGAGTCACTGTTGAAGCATTACAAAAGAGATAGGGTTAAGGCTTACCCAC 420
 Qy 379 CTGCTGTCAAGTACCACTAGTGGGTCTTCTGAGGAGGGAAGTCTCTGTGTTGCCAGCAG 438
 Db 421 CTGCTGTCAAGTACCACTAGTGGGTCTTCTGAGGAGGGAAGTCTCTGTGTTGCCAGCAG 480
 Qy 439 AGCTGTAAAGCAGCCCCCAGGATGTACCCCTCTGGGAGGCATATGCTAATCTGCATATGCA 498
 Db 481 AGCTGTAAAGCAGCCCCCAGGATGTACCCCTCTGGGAGGCATATGCTAATCTGCATATGCA 540
 Qy 499 GTCATGAGAGAAACACAGAGTTCACCTTCCAGACAGAGTCTGTAAGATACCTCGG 558
 Db 541 GTCATGAGAGAAACACAGAGTTCACCTTCCAGACAGAGTCTGTAAGATACCTCGG 600
 Qy 559 GCAGTCTCTGTTCTCAAAATGGATGACCATCTTCAAGTACCACCTAGCCCAATATGAC 618
 Db 601 GCAGTCTCTGTTCTCAAAATGGATGACCATCTTCAAGTACCACCTAGCCCAATATGAC 660
 Qy 619 AACGAATCAAGAAAGAACTATGCTGCTCCAGCCACCATCTTCAAGTACCACCTAGCGCAA 678

XX PF 22-OCT-2001; 2001WO-US51415.
 XX XX 23-OCT-2000; 2000US-242471P.
 PR XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA PI McAtee P;
 PI XX WPI; 2002-519317/55.
 DR DR P-PSDB; ABB76488.
 XX XX
 PT Assay for identifying compound that modulates the activity of Bruton's
 PT Tyrosine kinase, by contacting the cell expressing kinase with a test
 PT compound, and determining whether the compound modulates the kinase
 PT activity
 XX XX
 PS Disclosure; Page 13-14; 60pp; English.
 XX XX
 CC The present sequence is the nucleotide sequence of the murine
 CC Bruton's tyrosine kinase (BTK) gene encoding a 659-amino acid
 CC polypeptide (see ABB76488). BTK and intermediates in the BTK
 CC pathway are critical intermediates in the cytoskeletal
 CC rearrangement pathway leading to osteoclast activation. Mice
 CC deficient in BTK exhibit osteopenia, which can be reversed upon
 CC addition of multiple copies of the BTK gene in transgenic mice.
 CC Modulators of BTK activity and BTK intermediate activity are
 CC therefore useful in affecting osteoclast activity and bone
 CC resorption. Such modulators may be identified using assays of the
 CC present invention, and are expected to be useful in the treatment
 CC of osteoporosis and related disease states. BTK target validation
 CC studies on modulators may be carried out using conventional
 CC osteoporosis mouse models. The invention also includes the use of
 CC antisense therapy.
 XX XX
 SQ Sequence 2468 BP; 713 A; 559 C; 602 G; 594 T; 0 other;
 Query Match 20.1%; Score 494.6; DB 24; Length 2468;
 Best Local Similarity 64.08; Pred. No. 3.8e-125;
 Matches 746; Conservative 0; Mismatches 419; Indels 0; Gaps 0;
 QY 887 CTGAAGAGAGGAAACCTGGATGATTATGACTGGTTTGGTGTAAACATCTCCAGATCAC 946
 DB 941 CTGAAGCTGAGGACTCCATAGAGATGATGAGTGGTATTCACAGCATGATCGAAGTC 1000
 QY 947 AATCTGAACAGTACTCAGACAAAGGAAAGAGAGAGCATTTATGGTTAGAAATCGA 1006
 DB 1001 AAGCTGAGCAACTGCTAAAGCAAGAGGGGAAAGAGAGGTTTCATTGTTCAGAGACTCCA 1060
 QY 1007 GCCAAGTGGGAATCTACACAGTGCCTTATTTAGTAAGGCTGTCAATGATATAAAGGAA 1066
 DB 1061 GCAAGCTGGAATAATACCGTGTCTGTGTTTGTCTAATCTCTGGGGAGGCTCAAGGGG 1120
 QY 1067 CTGTCAACATATTACAGGTGCATACAAATGCTGAGAAACAAATTTACTGGCAGAAAAC 1126
 DB 1121 TGATCCGCCCATAGTTGTGTTCACGCCACAGAGCCAGTATTACCTGGCTGAGAAC 1180
 QY 1127 ACGTTTGTGATTCATTCGAAGCTTATTCATATCATCAACAAATTCAGCAGCATGA 1186
 DB 1181 ACCTCTTCAGCACCACATCCCTGAGCTCATTAACCTCAACAACTCTCAGCGCTCA 1240
 QY 1187 TCACACGGTCCGCCACCTGTGTCAACAAGGCCCAACAGGTCCTCGACTCTGTGCC 1246
 DB 1241 TATCCAGGCTGAATATCTGTGTCTTAACAAAAAAGCGCCCTTCTACTCAGGCC 1300
 QY 1247 TGGGAATGGAATCTGGGAAGTGAAGAGAGAGAGATTACCTCTTGAAGAGCTGGGA 1306
 DB 1301 TGGGCTATGATCATGGGAATTCATCCAAAGGACCTCACCTCTTGAAGAGCTGGGA 1360
 QY 1307 GTGCCAGTTTGGAGTGGTCCAGCTGGCAGTGGGAAGTGAAGGGCAGTATGATGTGCTGTTA 1366
 DB 1361 CTGGACAATTCGGTGTGCTGGAATATGGGAAGTGGAGGGGCAATATGATGTGCCATCA 1420

QY 1367 AGATGATCAGAGAGGCTCCATGTCAGAAAGATGAATCTTTTCAGGAGGCCAGACTATGA 1426
 DB 1421 AGATGATCAGAAAGGTTCCATGTCGGAGGATGAATTCATTCAAGAACCAAGTCATGA 1480
 QY 1427 TGAACCTAGCCATCCCAAGCTGGTTAAATTTCTATFGGAGTGTGTTCAAGGATACCCCA 1486
 DB 1481 TGAATCTTTCCATGAGAAAGCTGGTGCAGTGTGATGGCTGTGCAACCAACCCCA 1540
 QY 1487 TATACATAGTCACTGAATATATAGCAATGCTGCTCTGAATTTACCTGAGGAGTCAAG 1546
 DB 1541 TCTTCATCATCACCGAGTACATGGCTAATGGCTGCTCTTGAATCTTACCTGAGGAGATGC 1600
 QY 1547 GAAAGGACTTGAACCTTCCAGCTCTTAGAAATGCTAGCATGCTCTGTGAAGCATGG 1606
 DB 1601 GGCACCCCTCCAGACACAGAGCTGCTGAGATGTGCAAGATGCTGTGAAGCAATGG 1660
 QY 1607 CTTTCTTGGAGAGTCAACCAATTCATACCCGGGACTTGGCTGCTGCTGTAAGTCTTGGTG 1666
 DB 1661 AATACTTGGAGTCAAGAGCAGTTCTCTTACAGAGACCTGGCAGCTCGAACTGTTGGTAA 1720
 QY 1667 ACAGAGATCTCTGTGTGAAGTATCTGACTTTGGAATGACAAGGTATGTTCTTTGATGACC 1726
 DB 1721 ACGATCAAGGAGTGTGGAAGTATCTGACTTTGGCTGCTTAGGTATGCTCTTGTATGATG 1780
 QY 1727 AGTATGTCAGTTCAGTCGGAACAAAGTTTCCAGTCAAGTGTGTCAGCTCCAGAGGTGTTTC 1786
 DB 1781 AGTACACAGCTCTGTAGGCTCCAAAGTTTCCAGTCCGGTGTCTCCACAGAAAGTCTTA 1840
 QY 1787 ATTACTTCAATACAGCAGCAAGTCAGAGCTATGGGCAATTTGGGATCTGTATGTTGGAGG 1846
 DB 1841 TGTATAGCAAGTTTCAAGCAAAATCTGACATCTGGGCTTTTGGGGTTTAAATGTGGGAGA 1900
 QY 1847 TGTTCAGCTCTGGGAAGCAGCCCTATGACTTGTATGACAACTCCAGGTGTTCTGAAGG 1906
 DB 1901 TCTACTCTCTGGGAAGATGCGGTATGAGAGATTACTAACAGTGAAGACAGACACACA 1960
 QY 1907 TCTCCAGGCGCACAGGCTTTTACCGGCCCCACCTGGCATCGGACACCATCTACCATCA 1966
 DB 1961 TTGCTCAAGGCTTACGTCTCTACAGGCTCTATCTGGCATCAGAGAGGGTATATACCATCA 2020
 QY 1967 TGTACAGTCTGGCAGCAGCTTCCAGAAAGCGTCCCAACATTTTCAGCAACTCTCTGCTTT 2026
 DB 2021 TGTACAGTCTGGCAGCAGAAAGCAGATGAACGCTCTAGTTTCAAAATTTCTCTTGAAGTA 2080
 QY 2027 CCATTGACCACTTCGGGAAAAAGA 2051
 DB 2081 ACATTCTAGATGTGATGGATGAAGA 2105
 RESULT 7
 AAT45648
 ID AAT45648 standard; cDNA; 2505 BP.
 XX AC AAT45648;
 XX AC AAT45648;
 DT 25-MAR-2003 (updated)
 DT 04-FEB-1997 (first entry)
 XX XX
 DE Mouse haematopoietic-restricted tyrosine kinase cDNA.
 XX Haematopoietic; tyrosine kinase; autophosphorylation; growth; assay;
 KW transphosphorylation; differentiation; B cell progenitor kinase;
 KW hyperproliferative; allergy; non-neoplastic; autoimmune disease;
 XX cancer; ds.
 OS Mus sp.
 XX Key Location/Qualifiers
 FH 1..136
 FT 5'UTR /tag= a
 FT CDS 137..2116
 FT /tag= b
 FT 3'UTR 2117..2505


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FT polyA_signal /*tag= c 2458..2463
FT /*tag= d
FT polyA_site 2485
FT /*tag= e
XX US5550054-A.
XX 27-AUG-1996.
XX 21-FEB-1995; 95US-0391615.
XX 21-JAN-1993; 93US-0006449.
XX 04-DEC-1992; 92US-0985998.
XX 21-FEB-1995; 95US-0391615.
XX (REGC ) UNIV CALIFORNIA.
XX Rawlings D, Saffran D, Tsukada S, Witte O;
XX WPI; 1996-401601/40.
XX P-PSDB; AAW06708.
XX New haematopoietic restricted tyrosine kinase DNA - used to develop
XX products for modulating tyrosine kinase activity, e.g. for treating
XX neoplasia, auto-immune disease or allergy
XX Claim 2; Column 19-24; 26pp; English.
XX AAT45648 is a cDNA sequence encoding a murine haematopoietic-
XX restricted tyrosine kinase (TK) also known as B cell progenitor
XX kinase (BPK). The TK enzyme can be used to identify compounds that
XX inhibit or stimulate the expression and/or function of TK. The
XX TK is capable of autophosphorylation and transphosphorylation.
XX Modulators of TK activity can be used to treat neoplasia and
XX non-neoplastic hyperproliferative disease, e.g. allergy and
XX autoimmune disease. TK may also be used to determine cell-types
XX based on the nature and amount of TK present.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 2505 BP; 743 A; 559 C; 602 G; 601 T; 0 other;
Query Match 20.1%; Score 493; DB 17; Length 2505;
Best Local Similarity 63.9%; Pred No. 1.1e-124;
Matches 745; Conservative 0; Mismatches 420; Indels 0; Gaps 0;
QY 887 CTGAAGAAGAGGAAACCTGGATGATATGACTGTTGCTGGTAACATCTCCAGATCAC 946
DB 945 CTGAAGCTGAGGACTCCATAGAGATGTATGAGTGTATTCACAGCAGATGCTCAAGTC 1004
QY 947 AATCTGAACAGTTACTACAGACAAAGGAAAGAGAGGAGCAATTTATGGTTAGAAATCGA 1006
DB 1005 AAGCTGAGCAACTGCTAAGCAAGAGGAAAGAGGAGGTTTCATTGTCAGAGACTCCA 1064
QY 1007 GCCAAGTGGGAATPACACAGTGTCTTTATTTAGTAAGGCTGTGAATGATAAAAGGAA 1066
DB 1065 GCAAGCTGGAAATATACACCGTGTCTGTGTTGCTAAATATCTACTGGGAGCCTCAAGGG 1124
QY 1067 CTGTCAAAACATTACACAGTGTACAAATGCTTGAGAACAAATATATACCTGGCAGAAACT 1126
DB 1125 TGATCCGCCATTACCTGTGTGTTCCAGCCACAGAGCCAGTATTACCTGGCTGAGAAC 1184
QY 1127 ACTGTTTGTATTCATCCAAAGCTTATTCATATPACATCAACAAATTCAGAGGCATGA 1186
DB 1185 ACCTCTTCAGCACCACCTCCTGAGCTCATTAATACATCAACAACTCTGAGCCCTCA 1244
QY 1187 TCACAGGCTCCGACACCTGTGTCAACAAAGGCAAGGTCGCCAGCTGTGTGCC 1246
DB 1245 TATCCAGCTGAATATATCTGTGTCTAAACAAACAAACGCGCTTCTACTGCGAGCC 1304
QY 1247 TGGGAAATGGAATCTGGCAACTGAAAGAGAGAGATTACCTGTGTGAAGGAGCTGGGA 1306
DB 1305 TGGCTATGGATCATGGGAAATTTGATCCAAAGGAGCTCACCTTCTTGAAGGAGCTTGGGA 1364

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QY 1307 GTGGCAGGTTTGGAGTGGTCCAGCTGGGCAAGTGGAGGGCAGTATGATGTTGCTCTTA 1366
DB 1365 CTGGACAATTCGCTGTCGTAATATGGAAGTGGAGGGCCAAATATGATGTGCCATCA 1424
QY 1367 AGATGATCAAGAGGAGGCTCCATGTCAGAGATGAATTCCTTTTCAGGAGGCCAGACTATGA 1426
DB 1425 AGATGATCAGAGAAGGTTCCATGTCGAGGATGAATTCATTTGAAGAAGCCAAAGTCATGA 1484
QY 1427 TGAAACTCAGCCATCCCAAGCTGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCA 1486
DB 1485 TGAATCTTTCCCATGAGAAGCTGTCGAGTGTGATGCGCTGTCGACCAACAAACGCCCA 1544
QY 1487 TATACATAGTACTGAATATATATAAGCAATGGCTTGTGCTGAATACCTCAGGAGTCAAG 1546
DB 1545 TCTTCATCATCACCGAGTACATGGCTAATGGCTGCTCTTGAACCTACCTCAGGAGATGC 1604
QY 1547 GAAAGGACTTGAACCTTCCAGCTCTTAGAATATGCTACGATGCTGTGAAGGCATGG 1606
DB 1605 GGCACCGCTTCCAGACACAGCAGCTGCTTGAGATGTGCAAGATGCTGTGAAGCAATGG 1664
QY 1607 CCTTCTTGGAGAGTCAACCAATTCATACACCGGAGCTTGGCTGCTCGTAACCTGCTGGTGG 1666
DB 1665 AATACTTGGAGTCGAGAGCAGTCTTCCACAGACACCTGGCAGCTCGAAGCTGTTGGTAA 1724
QY 1667 ACAGAGATCTCTGTGTGAAAGTATCTGACTTTTGAATGACAAGGTATGTTCTTGATGACC 1726
DB 1725 ACGATCAAGGAGTGTGAAAGTATCTGACTTTTGGCCTGCTAGGTATGCTCTTCATGATG 1784
QY 1727 AGTATGTCAGTTCAGTCGGAACAAAGTTTCCAGTCAAGTGGTCCAGCTCCAGAGTGTTC 1786
DB 1785 AGTACACCGCTCTGTAGGCTCCAAAGTTTCCAGTTCGCTGGTCTCCACAGAGTGTCTTA 1844
QY 1787 ATTACTTCAAAATACACAGCAGCAGTATGAGTATGGGATTTGGGATCCTGATGTTGGAGG 1846
DB 1845 TGTATAGCAAGTTCACAGCAATCTGACATCTGGGCTTTTGGGCTTTTATGTTGGAGA 1904
QY 1847 TGTTCAGCTGGGGAAGCAGCCCTATGACTTTGATGACAACCTCCAGAGTGGTGTCTGAAGG 1906
DB 1905 TCTACTCCCTGGGGAAGATGCCGTATGAGAGATTTACTAACAGTGTAGACAGCAGAACACA 1964
QY 1907 TCTCCAGGCGCACAGGCTTTACCGGCCACCTGGCATCGGACACCATCTACACAGATCA 1966
DB 1965 TTGCTCAAGCTTACCTCTCTACAGCCCTCATCTGGCATCAGAGAGGTTATATACCATCA 2024
QY 1967 TGTACAGCTGCTGGCAGCAGCTTCCAGAAAAGCGTCCCATTTTCAGCAACTCCTGTCTT 2026
DB 2025 TGTACAGCTGCTGGCAGCAGAGAGCAGATCAACGCTCCTAGTTTTCAAAATTTCTCTTGAGTA 2084
QY 2027 CCATTGAACCACTTCGGGAAAAGA 2051
DB 2085 ACATTCTAGATGTGATGGATGAAGA 2109
RESULT 8
ABK85707
ID ABK85707 standard; DNA; 1365 BP.
XX
AC ABK85707;
XX
DT 20-AUG-2002 (first entry)
XX
DE DNA encoding truncated Tec Kinase Btk.
XX
KW Tec kinase; pleckstrin-homology domain; Tec homology domain;
KW inflammation; asthma; allergic rhinitis; arthritis; rheumatoid arthritis;
KW adult respiratory distress syndrome; osteoarthritis; uveitis;
KW inflammatory eye condition; inflammatory bowel condition;
KW Crohn's disease; ulcerative colitis; periodontal disease; oesophagitis;
KW inflammatory skin condition; psoriasis; eczema; dermatitis; Btk;
XX gene; ds; human.
XX Homo sapiens.
OS

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XX Key Location/Qualifiers
 FH CDS 1..1365
 FT /*tag= a
 FT /product= "Truncated Btk"
 FT /note= "tec kinase"
 XX W0200234899-A2.
 XX
 XX 02-MAY-2002.
 XX
 XX 17-OCT-2001; 2001WO-EPI1949.
 XX
 XX 20-OCT-2000; 2000GB-0025804.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Sims MJ, Hayes DJ;
 XX
 XX WPI; 2002-471439/50.
 DR P-PSDB; AAU98426.
 XX
 XX New truncated Tec kinase polypeptide useful for identification of a
 PT compound which modulates the activity of the polypeptide for treating
 PT inflammatory conditions such as asthma, rheumatoid arthritis, and
 PT uveitis -
 XX
 XX Claim 13; Fig 9; 38pp; English.
 XX
 CC The invention describes a truncated Tec kinase polypeptide (I) having a
 CC Tec kinase amino acid sequence truncated by a minimum of the amino acids
 CC constituting the N-terminal pleckstrin-homology (PH) domain and a portion
 CC of the Tec homology (TH) domain including a proline rich region up to but
 CC not including the amino acids constituting the kinase domain. A compound
 CC (II) which modulates Tec activity is useful in treatment of a disorder
 CC such as inflammation that is responsive to modulation of Tec
 CC kinase activity. (I) is useful for screening for targets for the
 CC identification and development of new pharmaceutical agents, including
 CC agonists and antagonists of Tec kinases, which may be useful in therapy.
 CC The nucleic acid (II) encoding (I) is useful for treating inflammatory
 CC diseases such as asthma, allergic rhinitis, adult respiratory distress
 CC syndrome, arthritic conditions such as rheumatoid arthritis,
 CC osteoarthritis, inflammatory eye conditions such as uveitis, inflammatory
 CC bowel conditions such as Crohn's disease, ulcerative colitis, periodontal
 CC disease, oesophagitis, and inflammatory skin conditions such as
 CC psoriasis, eczema and dermatitis. (I) is suitable for screening methods
 CC as they do not need to be pre-activated by phosphorylation. In vivo, Tec
 CC kinases need to be phosphorylated by other kinases in order to activate
 CC the enzyme, while pre-activation by phosphorylation is commonly required
 CC in assays. The removal of the need to pre-activate (I) offers a
 CC simplification for the assay. A further advantage of (I) is the provision
 CC of an assay that is robust as: it is possible to generate large amounts
 CC of truncated enzyme which are stable over a long time and the assay gives
 CC a high frequency of comparable results upon repeat testing. This sequence
 CC encodes a truncated construct of the Tec kinase Btk.
 XX
 SQ Sequence 1365 BP; 395 A; 301 C; 344 G; 325 T; 0 other;
 Query Match 19.78; Score 485; DB 24; Length 1365;
 Best Local Similarity 63.5%; Pred. No. 1.2e-122;
 Matches 740; Conservative 0; Mismatches 425; Indels 0; Gaps 0;
 QY 887 CTGAAGAAGAGGAAACCTGGATGATTGACTGGTTTGGTAAACATCTCCAGATCAC 946
 DB 194 CTGAACGGGAGACTCCATAGAATGTATGAGTGGTATTCGAACACATGACTCGGAGTC 253
 QY 947 AATCTGAACAGTTACTCAGCAAGGAAAGGAGGAGGATTTATGGTTAGAAATTCGA 1006
 DB 254 AGGCTGAGCAACTGCTAAAGCAAGAGGGGAAAGAGGAGGTTTCATTGTGACGACTCCA 313
 QY 1007 GCCAAGTGGGAATGTACACAGTGTCTTATTTAGTAGGCTGTGAATGATAAAAGGAA 1066
 DB 314 GCAAGCTGGCAATATACAGTGTCTGTGTTTGTGTAATCCACAGGGGACCTCAAGGGG 373

RESULT 9
 ABN83857
 ID ABN83857 standard; DNA; 2560 BP.

QY 1067 CTGTCAACAACATPACACAGTGCATACAAATGCTGAGAACAAATATTACCTGGCAGAAAACCT 1126
 DB 374 TGATACGTCATTATGTTGTGTGTTCCACACCTCAGAGCCAGTATTACCTGGCTGAGAAGC 433
 QY 1127 ACTGTTTGTGATTCATCCAAAGCTTATTTCATCATCAACACATCAACAGGACATCA 1186
 DB 434 ACCTTTTCAGCACCATCCCTGAGCTCATTAACCATCAGCACAACTCTCGAGGACATCA 493
 QY 1187 TCACACGGCTCCGCCACCCCTGTGTCAACAAAGGGCCAAAGTCCCGACTCTGTGTGCC 1246
 DB 494 TATCCAGGCTCAAAATATCCAGTGTCTCAACAAACAGAAATGCACCTTCCACTCGAGGCC 553
 QY 1247 TGGGAAATGGAATCTGGGAACCTGAAAGAGAGATTAACCTGTTTGAAGAGCTGGGAA 1306
 DB 554 TGGGATACGGATCATGGAATATGATCCAAAGGACCTGACCTTCTTGAAGGAGCTGGGA 613
 QY 1307 GTGCCAGTTTGGGAGTGTCCAGCTGGGCAAGTGGGAAGGGCAGTATGATGTTGCTGTA 1366
 DB 614 CTGGACAATTTGGGGTAGTGAAGTATGGGAATGGAGAGGCCAGTACGACGTGGCCATCA 673
 QY 1367 AGATGATCAAGGAGGGCTCCATGTCAGAAAGATGAATTTCTTCAGGAGGCCACAGACTATGA 1426
 DB 674 AGATGATCAAGAGAGGCTCCATGCTGAAGATGAATTCATTGAAGAGCCAAAGTCAATGA 733
 QY 1427 TGAACATCAGCCATCCCAAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGGAATACCCCA 1486
 DB 734 TGAATCTTTCCCATGAGAAGCTGGTGCAAGTTGTATGGGCTCTGCACCAAGACGCCCA 793
 QY 1487 TATACATAGTACATGAATATATATAGCAATGCTGCTTCTGTAATTAACCTGAGGAGTCAAG 1546
 DB 794 TCTTTCATCATCATCAGTACATGGCCAATGGCTGCTCTTCTTCACTACCTGAGGAGATGC 853
 QY 1547 GAAAGGACTTGAACCTTCCAGCTCTTAGAAATGTGTACGATGCTCTGTGAAGGATGG 1606
 DB 854 GCCACCGCTTCCAGACTCAGCAGCTGTAGAGATGTGCAAGGATGTCTGTGAAGCCATGG 913
 QY 1607 CTTTCTTGGAGAGTCAACCAATTCATACACCGGACTTGGCTGCTGCTGAATTAACCTCTTGGTGG 1666
 DB 914 AATACCTGGAGTCAAGCAGTTCCTTCCACGAGACCTGCGAGCTCGAACTGTTTGGTAA 973
 QY 1667 ACAGAGATCTCTGTGTGAAGTATGACTTTTGAATGACAAAGGATGTTTCTTGATGACC 1726
 DB 974 ACGATCAAGGAGTGTGTTAAAGTATCTGATTTGGGCTGTCCAGGTATGTCTCTGGATGATG 1033
 QY 1727 AGTATGTCAGTTCAGTGGGAACAAGTTTCCAGTCAAGTGTGTCAGTCCAGAGGTGTTTC 1786
 DB 1034 AATACAAAGCTCAGTAGGCTCCCAATTTCCAGTCCGGTGGTCCCGACCGGAAGTCTCTGA 1093
 QY 1787 ATTACTTCAAAATACAGCAGCAAGTCAAGTATGGGCATTTTGGGATCTCTGATGTGGGAG 1846
 DB 1094 TGTATAGCAAGTTCAGCAGCAAACTGACATTTGGGCTTTTGGGCTTTTGTGATGTGGGAA 1153
 QY 1847 TGTTCAGCTCGGGAAGCAGCCCTATGACTTGTATGACAACTCCAGGTTGGTTCTGAAGG 1906
 DB 1154 TTTACTCCCTGGGGAAGATGCCATATGAGAGATTTTACTAAACAGTGTGCTGTGAACACA 1213
 QY 1907 TCTCCAGGGCCACAGGCTTTACCGGCCCTTACCGGCTTCCAGTCCGACACCATCTTACCAGATCA 1966
 DB 1214 TTGCCCCAAGGCTTACGCTCTACAGGCTCTATCTGGCTTTCAGAGAGGTATATACCATCA 1273
 QY 1967 TGTACAGTGTGTGCACGAGCTTCCAGAAAAGGCTCCCAACATTTTCAGCAACTCTCTGCTT 2026
 DB 1274 TGTACAGTGTGTGCATGAGAAAGCAGATGAGCGTCCCACTTTTCAAAATTTCTTCTGAGCA 1333
 QY 2027 CCATTGAACCACTTCGGGAAAAAGA 2051
 DB 1334 ATATTCTAGATGTCTATGGATGAAGA 1358

XX AC ABN83857;
 XX DT 10-SEP-2002 (first entry)
 XX DE Human Bruton's tyrosine kinase gene.
 XX KW Bruton's tyrosine kinase; BTK; enzyme; human; osteoporosis;
 XX KW osteoclast; diagnosis; gene therapy; gene; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 133..2112
 XX FT /*tag= a
 XX FT /product= "BTK"
 XX PN WO200238797-A2.
 XX XX 16-MAY-2002.
 XX PF 22-OCT-2001; 2001WO-US51415.
 XX PR 23-OCT-2000; 2000US-242471P.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI McAttee P;
 XX DR WPI; 2002-519317/55.
 XX DR P-PSDB; ABB76487.
 XX PT Assay for identifying compound that modulates the activity of Bruton's
 XX PT Tyrosine kinase, by contacting the cell expressing kinase with a test
 XX PT compound, and determining whether the compound modulates the kinase
 XX PT activity
 XX PS Disclosure; Page 11-12; 60pp; English.
 XX CC The present sequence is the nucleotide sequence of the human
 XX CC Bruton's tyrosine kinase (BTK) gene encoding a 659-amino acid
 XX CC polypeptide (see ABB76487). BTK and intermediates in the BTK
 XX CC pathway are critical intermediates in the cytoskeletal
 XX CC rearrangement pathway leading to osteoclast activation. Mice
 XX CC deficient in BTK exhibit osteopenia, which can be reversed upon
 XX CC addition of multiple copies of the BTK gene in transgenic mice.
 XX CC Modulators of BTK activity and BTK intermediate activity are
 XX CC therefore useful in affecting osteoclast activity and bone
 XX CC resorption. Such modulators may be identified using assays of the
 XX CC present invention, and are expected to be useful in the treatment
 XX CC of osteoporosis and related disease states. BTK target validation
 XX CC studies on modulators may be carried out using conventional
 XX CC osteoporosis mouse models. The invention also includes the use of
 XX CC antisense therapy.
 XX SQ Sequence 2560 BP; 758 A; 564 C; 626 G; 612 T; 0 other;
 Query Match 19.7%; Score 485; DB 24; Length 2560;
 Best Local Similarity 63.5%; Pred. No. 1.7e-122;
 Matches 740; Conservative 0; Mismatches 425; Indels 0; Gaps 0;
 QY 887 CTGAGAGAGAGAAACCTGGATGATATGACTGGTTTCGTGTAACATCTCCAGATCAC 946
 Db 941 CTGAAGCAGAGAGATCCATGAAATATGATGATGTTCCAAACACATGACTCGGAGTC 1000
 QY 947 AATCTGAACAGTTACTCAGACAAAGGAAAGAGGAGGAGCATTTATGCTTAGAATTGGA 1006
 Db 1001 AGGCTGAGCACTGCTTAAGCAGAGAGGAAAGAGGAGGTTTCATTGTCAGACATCCA 1060
 QY 1007 GCCAAGTGGGAATACACAGTGTCTTATAGTAAAGGCTGTGTAAGTATAAAGGAA 1066
 Db 1061 GCAAAGCTGGCAATATACAGTGTCTGTTTGTGTAATCCACAGGGGACCTCAGGGG 1120

QY 1067 CTGTCAAACATTTACCACGCTGCATACAAATGCTGAGAACAAATTTATACCTGGCAGAAACT 1126
 Db 1121 TGATACGTCATTTATGTTGTGTTCACACACCTCAGAGCCAGTATTACCTGGCTGAGAAGC 1180
 QY 1127 ACTGTTTGTGATTCCATTTCCAAAGCTTATTTCATTATCATCAACAATTCAGCAGGATGA 1186
 Db 1181 ACCTTTTCAGCACCATCTCCAGCTCATTTAACTACCATCAGCACACTCTGAGGACTCA 1240
 QY 1187 TCACACGGCTCCGCCACCTGTGTCAACAAAGGCCCAACAGGTCCCGACTCTGTGTGCC 1246
 Db 1241 TATCCAGGCTCAAAATATCCAGTGTCTCAACAAACAAAGAAATCCACCTTCACCTGCAGGCC 1300
 QY 1247 TCGGAATGGAATCTGGGAACCTGAAAGAGAGAGATTTACCTGTTTGAAGGACCTGGGA 1306
 Db 1301 TGGGATACGGATCATCGGAAATTTGATCCAAAGAGACCTGACCTTCTTGAAGGAGCTGGGA 1360
 QY 1307 GTGGCAGTGTGGAGTGGTCCAGCTGGGCAAGTGGAAAGGCGCATGATGTTGCTGTGA 1366
 Db 1361 CTGGACAATTTGGGGTAGTGAAGTATGGGAATGGAGAGCCAGTACGACGTGCCATCA 1420
 QY 1367 AGATGATCAAGAGGGCTCCATGTGAGAGATGAATTTCTTCAGGAGGCCAGACTATGA 1426
 Db 1421 AGATGATCAAGAGGGCTCCATGTGAGAGATGAATTTCTTCAGGAGGCCAGACTATGA 1480
 QY 1427 TGAACCTCAGCATCCCAAGCTGTTTAAATTTCTATGAGTGTGTTCAAGAGATACCCCA 1486
 Db 1481 TGAATCTTTCCCATGAGAAAGCTGGTGCAGTTGTATGGCTGTGCACCAAGCAGCGGCCCA 1540
 QY 1487 TATACATAGTGACTGAATATATAAGCAATGCGTGTGCTGAATTTACCTGAGGAGTCACG 1546
 Db 1541 TCTTCATCATCACTGAGTACATGGCAATGGCTGCTCTGAACTACCTGAGGAGATGC 1600
 QY 1547 GAAAGAGACTTGAACCTCCCAAGCTCTTAGAATGTGCTACAGTGTCTGTGAAGGATGG 1606
 Db 1601 GCCACCGCTTCCAGACTCAGCAGCTGCTAGAGATGTGCAAGGATGCTGTGAAGGATGG 1660
 QY 1607 CTTCTCTGAGAGTCAACCAATTCATACACCGGAGCTTGGCTGCTCCTCACTGCTGCTGG 1666
 Db 1661 AATACCTGGAGTCAAGAGCTTCTTCACCGAGAGCTGGCAGCTCGAAACTGTTTGGTAA 1720
 QY 1667 ACAGAGATCTCTGTGTGAAAGTATCTGACTTTGGAAATGACAGGATGATGTTTGTGATGACC 1726
 Db 1721 ACGATCAAGGAGTCTGTTAAAGTATCTGATTTTCGGCTGTCCAGGTATGCTCTGATGATG 1780
 QY 1727 AGTATGTCAGTTCAGTCGGAACAAAGTTTCCAGTCAAGTGTGTCAGCTCAGAGGTTGTTTC 1786
 Db 1781 AATACACAAAGCTCAGTAGGCTCCAAATTTCCAGTCCGGTGGTCCCCACCGGAAGTCTCTGA 1840
 QY 1787 ATTACTTCAATACAGCAGCAGTCAAGTGTGAGTATGGCATTTGGGATCCTGATGTTGGGAGG 1846
 Db 1841 TGTATAGCAAGTTCAGCAGCAAAATCTGACATTTGGGCTTTTGGGGTTTGTGATGTTGGAAA 1900
 QY 1847 TGTTCAGCTTGGGGAAGCAGCCCTATGACTTGTATGACAACTCCCAAGTGGTTCCTGAAGG 1906
 Db 1901 TTTACTCTCTGGGAGAGATGCCATATGAGAGATTTACTAACAGTGAAGTCTGTCACACA 1960
 QY 1907 TCTCCAGGGCCACAGGCTTTTACCGGCCCACTGGCATCGGACACCACTTACAGATCA 1966
 Db 1961 TTGCCAAGGCTTACGTCTCTACAGGCTCATCTGCTTTCAGAGAAGGTATATACCATCA 2020
 QY 1967 TGTACAGCTGCTGGCAGCAGCTTCCAGAAAAGCGTCCCACTTTCAGCAACTCTCTGCTT 2026
 Db 2021 TGTACAGTGTGGCATGAGAAAGCAGATGAGCGTCCCACTTTCAAATTTCTTCTGAGCA 2080
 QY 2027 CCATTGAACCACTTCGGGAAAAGA 2051
 Db 2081 ATATTCTAGATGTCATGATGAAGA 2105

RESULT 10
 AAS14047
 ID AAS14047 standard; cDNA; 2582 BP.
 XX

AA570719 standard; cDNA; 3650 BP.
AA570719;
13-FEB-2002 (first entry)
DNA encoding novel human diagnostic protein #6523.
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
Homo sapiens.
W0200175067-A2.
11-OCT-2001.
30-MAR-2001; 2001WO-US08631.
31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
(HYSE-) HYSEQ INC.
Dmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
P-PSDB; ABG08532.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -
Claim 1; SEQ ID No 6523; 103pp; English.
The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 3650 BP; 1083 A; 726 C; 884 G; 957 T; 0 other;
Query Match 16.08; Score 392.8; DB 23; Length 3650;
Best Local Similarity 58.98; Pred. No. 4.8e-97;
Matches 698; Conservative 0; Mismatches 482; Indels 6; Gaps 1;
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AAS14048
ID AAS14048 standard; cDNA; 3593 BP.

AC AAS14048;

XX 18-DEC-2001 (first entry)

DE Human cDNA encoding protein tyrosine kinase, Tec.

XX Immunosuppressive; antiinflammatory; osteopathic; antirheumatic;
KW antiarthritic; dermatological; antipsoriatic; antiasthmatic; cytostatic;
KW cardiatic; antiarteriosclerotic; vasotropic; cerebroprotective;
KW neuroprotective; nontropic; ophthalmological; immunosuppressive;
KW hepatotropic; virucide; anti-HIV; immunomodulator; antithyroid; sepsis;
KW septic shock; inflammation; Crohn's disease; rheumatoid arthritis;
KW leukopenia; osteoarthritis; spondyloarthropathy; psoriatic arthritis;
KW severe steroid resistant asthma; pulmonary fibrosis; myocarditis;
KW atherosclerosis; angina; vasculitis; reperfusion injury; infarction;
KW stroke; multiple sclerosis; Alzheimer's disease; Graves ophthalmopathy;
KW psoriasis; transplant rejection; acute alcoholic hepatitis; fibrosis;
KW HIV; human immunodeficiency virus; cachexia; erythema nodosum leprosum;
KW borreliosis; meningococcal septicaemia; cancer; Human; Tec; ss;
KW antibacterial; protein tyrosine kinase.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 57..1913

XX FT /*tag= a

XX FT /product= "Tec"

XX PN WO200166107-A2.

XX PD 13-SEP-2001.

XX PF 06-MAR-2001; 2001WO-GB00949.

XX PR 06-MAR-2000; 2000GB-0005345.

XX (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.

XX PI Foxwell BMJ;

XX WP1; 2001-602596/68.

XX P-PSDB: AAU09010.

XX Treating condition associated with cytokine production in a mammal,

XX e.g. sepsis, septic shock, inflammation and Crohn's disease, comprises

XX administering an inhibitor of a member(s) of the Tec family of protein

XX tyrosine kinases

XX Claim 23; Fig 13; 78pp; English.

XX The invention relates to the use of inhibitors of the Tec family of
CC protein tyrosine kinases to treat a condition associated with cytokine
CC production in a mammal. The Tec family members are e.g. Bruton's
CC tyrosine kinase (Btk), Tec, Itk, Txk or Bmx. The condition is especially
CC sepsis, septic shock, inflammation, Crohn's disease or a condition
CC induced by TLR (Toll related receptor) ligand, LPS (lipopolysaccharide),
CC zymosan or Gram-negative bacteria. The method may also be used for
CC treating rheumatoid arthritis. Biological effects of LPS include fever,
CC circulatory disturbances and vascular hypersensitivity to adrenergic
CC drugs, leukopenia typically followed by leucocytosis, non-specific
CC stimulation of B-lymphocytes to undergo blast transformation and
CC proliferation, lethal toxicity and non-specific tolerance to endotoxin
CC through repeated exposure to LPS. LPS also causes an increase in
CC production of cytokines e.g. TNF. Conditions associated with IL-1beta
CC and TNFalpha osteoarthritis, spondyloarthropathy, psoriatic arthritis,
CC severe steroid resistant asthma, pulmonary fibrosis, myocarditis,
CC atherosclerosis, angina with high CRP/IL-6, vasculitis, reperfusion
CC injury, infarction, stroke, multiple sclerosis, Alzheimer's disease,
CC Graves ophthalmopathy, psoriasis, transplant rejection, acute alcoholic
CC hepatitis, fibrosis. Other conditions for which inhibitors of Tec

CC family PKs may be used include HIV (human immunodeficiency virus
CC infection, cachexia, erythema nodosum leprosum, borreliosis, or
CC meningococcal septicaemia, cancer, such as breast cancer, ovarian cancer
CC or colon cancer. Many other examples of diseases are given in the
CC specification. The present sequence encodes human Tec.

XX Sequence 3593 BP; 1070 A; 702 C; 865 G; 956 T; 0 other;

XX Query Match 15.8%; Score 388; DB 22; Length 3593;

XX Best Local Similarity 59.68; Pred. No. 9.9e-96;

XX Matches 674; Conservative 0; Mismatches 450; Indels 6; Gaps 1;

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QY 959 TACTCACAAAAAGGAAAGGACGACATTTATGCTTAGAAATTCGAGCCAAAGTGGAA 1018

DB 835 TCCCTCCAGTGAAGATAAAGAGGTGGTTTATGGTAAGGATTCACAGTCAACAGGCT 894

QY 1019 TGACACAGTCTCCTTATTTAGTAAGGCTGTGAATGATAAAAAAGGAATCTGCAACAT 1078

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QY 1253 ATGGAATCTGGGAATGAAAGAGAGAGATTTACCTTGTGTAAGGAGCTGGGAAGTGCC 1312

DB 1135 ATGAGAAATGGGAGATTAAACCTTTTATGAGGAAATGGGAAGTGGGAAGTGAC 1194

QY 1313 AGTTGGAGTGTCCAGCTGGGCAAGTGGGAAGGCGCAGTATGATGCTGTAGATGA 1372

DB 1195 TGTTGGAGTGTGGAGCTTGGCAAAATGGCGAGGCCAGTCAAAAGTCCCAATCAAGGTA 1254

QY 1373 TCAAGGAGGCTCCATGTCAAGATGAATTTTTCAGGAGGCCACAGACTATGATGAAC 1432

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 Qy 1973 GCTGCTGSCAGAGCTTCCAGAAAGGCTCCACATTTTCAGCAACTCTCTG 2022
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RESULT 15

ABK85703
 ID ABK85703 standard; DNA; 1368 BP.

XX AC ABK85703;

XX DT 20-AUG-2002 (first entry)

XX DE DNA encoding truncated Tec kinase Itk.

XX KW Tec kinase; pleckstrin-homology domain; Tec homology domain;
 KW inflammation; asthma; allergic rhinitis; arthritis; rheumatoid arthritis;
 KW adult respiratory distress syndrome; osteoarthritis; uveitis;
 KW inflammatory eye condition; inflammatory bowel condition;
 KW Crohn's disease; ulcerative colitis; periodontal disease; oesophagitis;
 KW inflammatory skin condition; psoriasis; eczema; dermatitis; Itk;
 KW gene; ds; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 7..1362
 XX FT /*tag= a
 XX FT /product= "Truncated Itk"
 XX FT /note= "Tec kinase"

XX PN WO200234899-A2.

XX PD 02-MAY-2002.

XX PF 17-OCT-2001; 2001WO-EP11949.

XX PR 20-OCT-2000; 2000GB-0025804.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Sims MJ, Hayes DJ;

XX DR WPI; 2002-471439/50.

XX DR P-PSDB; AAU98425.

XX PT New truncated Tec kinase polypeptide useful for identification of a
 PT compound which modulates the activity of the polypeptide for treating
 PT inflammatory conditions such as asthma, rheumatoid arthritis, and
 PT uveitis.

XX PS Claim 11; Fig 2; 38pp; English.

XX CC The invention describes a truncated Tec kinase polypeptide (I) having a
 CC Tec kinase amino acid sequence truncated by a minimum of the amino acids
 CC constituting the N-terminal pleckstrin-homology (PH) domain and a portion
 CC of the Tec homology (TH) domain including a proline rich region up to but
 CC not including the amino acids constituting the kinase domain. A compound
 CC (II) which modulates Tec activity is useful in treatment of a disorder
 CC such as inflammation that is responsive to modulation of Tec
 CC kinase activity. (I) is useful for screening for targets for the
 CC identification and development of new pharmaceutical agents, including

CC agonists and antagonists of Tec kinases, which may be useful in therapy.
 CC The nucleic acid (II) encoding (I) is useful for treating inflammatory
 CC diseases such as asthma, allergic rhinitis, adult respiratory distress
 CC syndrome, arthritic conditions such as rheumatoid arthritis,
 CC osteoarthritis, inflammatory eye conditions such as uveitis, inflammatory
 CC bowel conditions such as Crohn's disease, ulcerative colitis, periodontal
 CC disease, oesophagitis, and inflammatory skin conditions such as
 CC psoriasis, eczema and dermatitis. (I) is suitable for screening methods
 CC as they do not need to be pre-activated by phosphorylation. In vivo, Tec
 CC kinases need to be phosphorylated by other kinases in order to activate
 CC the enzyme, while pre-activation by phosphorylation is commonly required
 CC in assays. The removal of the need to pre-activate (I) offers a
 CC simplification for the assay. A further advantage of (I) is the provision
 CC of a truncated enzyme which is stable over a long time and the assay gives
 CC a high frequency of comparable results upon repeat testing. This sequence
 CC encodes a truncated construct of the Tec kinase Itk.

XX SQ Sequence 1368 BP; 370 A; 302 C; 374 G; 322 T; 0 other;

Query Match 15.7%; Score 385.4; DB 24; Length 1368;
 Best Local Similarity 59.5%; Pred. No. 3e-95;
 Matches 691; Conservative 0; Mismatches 461; Indels 9; Gaps 2;

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 Qy 959 TACTCAGACAAAGGAAAGAGGAGCATTTATGGTTAGAAATTCGAGCCAAAGTGGGAA 1018
 Db 254 TTCCTTTGGACACAGGCAAGAGAGCCCTTCATGTTAAGGATTTCCAGGATCGAGGAA 313
 Qy 1019 TGTACACAGTGTCTTTATTAGTAAGGC---TGTGAATGATAAAAAGGAAGTGTCAAC 1075
 Db 314 CATACACCGTGTCTGTTTTTCCACCAAGGCTGTTGTAAGTGAGAACAAATCCCTGTATAAGC 373
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 Db 374 ATTATCACATCAAGGAAACAAATGATCAATCCCTAAGCGATACTATGCGTGAAGATATG 433
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 Qy 1310 GCCAGTTTGGAGTGGTCCAGCTGGCAAGTGGGAAGGGCAGTATGATGTTGTTTAAAGA 1369
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 Qy 1550 AAGGACTTGAACCTTCCAGCTCTTAGAAATATGCTAGCATGTCTGTGAAGGAGCTAGGCT 1609
 Db 854 GACCTTTTGTGTCAGAGAGCCCTGCTGGCATGTGTGTGATGTGTGTGAGGCGATGGCT 913
 Qy 1610 TCTTGGAGAGTCAACCAATTCATACACCGGAGTCTGGCTGCTGCTGAATCTGCTGGTGAACA 1669


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Db 1334 TGGCTGAAATTCAGAAATCAG 1354
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GenCore version 5.1.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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30	360	14.7	380	9 <th>AI500626</th> <th>AI500626 tn98903.x</th>	AI500626	AI500626 tn98903.x
31	359.6	14.6	4155	11 <th>AK037554</th> <th>AK037554 Mus muscu</th>	AK037554	AK037554 Mus muscu
32	356	14.5	1033	13 <th>BQ429846</th> <th>BQ429846 AGENCOURT</th>	BQ429846	BQ429846 AGENCOURT
33	346	14.1	1355	13 <th>BQ714415</th> <th>BQ714415 AGENCOURT</th>	BQ714415	BQ714415 AGENCOURT
34	344.8	14.0	961	13 <th>BU461627</th> <th>BU461627 AGENCOURT</th>	BU461627	BU461627 AGENCOURT
35	344	14.0	533	10 <th>BF898833</th> <th>BF898833 IL0-WT028</th>	BF898833	BF898833 IL0-WT028
36	335.8	13.7	459	9 <th>AA187327</th> <th>AA187327 zp60a08.s</th>	AA187327	AA187327 zp60a08.s
37	323.4	13.2	533	10 <th>BE749703</th> <th>BE749703 200748 MA</th>	BE749703	BE749703 200748 MA
38	315.4	12.8	1039	12 <th>BM478046</th> <th>BM478046 AGENCOURT</th>	BM478046	BM478046 AGENCOURT
39	308	12.5	328	9 <th>AI382692</th> <th>AI382692 tc61b08.x</th>	AI382692	AI382692 tc61b08.x
40	304.4	12.4	478	10 <th>BE623796</th> <th>BE623796 ut22h09.y</th>	BE623796	BE623796 ut22h09.y
41	289	11.8	312	14 <th>Z40071</th> <th>Z40071 HSC1Q6122.n</th>	Z40071	Z40071 HSC1Q6122.n
42	283	11.5	288	9 <th>AW512350</th> <th>AW512350 xx73e10.x</th>	AW512350	AW512350 xx73e10.x
43	282.2	11.5	962	10 <th>BF795127</th> <th>BF795127 602256462</th>	BF795127	BF795127 602256462
44	277.2	11.3	723	9 <th>AJ395612</th> <th>AJ395612 AGENCOURT</th>	AJ395612	AJ395612 AGENCOURT
45	271.8	11.1	758	14 <th>CB310787</th> <th>CB310787 AGENCOURT</th>	CB310787	CB310787 AGENCOURT

ALIGNMENTS

RESULT 1
AK040936
LOCUS
DEFINITION
AK040936
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530048A03 product:BMX non-receptor
tyrosine kinase, full insert sequence.

ACCESSION
AK040936

VERSION
AK040936.1 GI:26334070

KEYWORDS
HTC: CAP trapper.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
1
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
Carninci, P. and Hayashizaki, Y.

TITLE
High-efficiency full-length cDNA cloning

JOURNAL
Meth. Enzymol. 303, 19-44 (1999)

MEDLINE
99279253

PUBMED
10349636

REFERENCE
2

AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

PUBMED
20499374

PUBMED
11042159

QY	547	AAGATACCTCGGCGAGTTCCTGTTCTCAAAATGGATGCACCATCTTCAAGTACCACCTCTA	606
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QY	607	GCCCAATATGACAAAGAAATCAAGAAATACTATGCTCCAGCCACCATCTTCAAGTACC	666
Db	730	CCC	732
QY	567	AGTCTAGGGCAATATGACAGCAACTCAAGAAATCTATGCTCCAGCCCAAACTTCAAC	726
Db	733	-----CAATATGACAGCTATTTCAAGAAAGTTGTGTTCCAGCCCAACAGCAAC	783
QY	727	ATGCAGTATATTCAAAGGAGAGACTTCCCTGCTGCTGGTGGCAAGTAAAGAACTGAAAGT	786
Db	784	ATACGCTATATTCAAAGGAGAGACTGCCCCGCTGCTGCTGGCAAGTAAAGAAACTGAAA	840
QY	787	AGCAGCAGCAGTGAAGATGTTGCAAGCAGTAACCAAAAGAAAGAAAT- - -GTGAATCAC	843
Db	841	-----ACGAGGAGAGACATTTGCATGCAGTAACCAACTGGAAAGAAATATCGCTCTCAC	894
QY	844	ACCACCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAAGAGAGAAAC	903
Db	895	AGCACCTCAAGATGTCATGGGATTCCTGAGTCAAGTTCATCAGAAGAGAGAAAT	954
QY	904	CTGATGATATGACTGGTTTCTGCTGGTAACTCTCCAGATCACAACTCTGAACAGTTACTC	963
Db	955	CTGATGTTATGACTGGTTTCTGCTGGGAATATATCTCCAGGTCACAATCTGAGCAGTTACTG	1014
QY	964	AGACAAAGGAGAAAGAGAGCATTTATGTTAGAAATTCGAGCCAAAGTGGGAATGTAC	1023
Db	1015	AGACAAAGGAGAAAGAGAGCATTTATGTTGCGAATTCAGCCAGATGGGAATGTAC	1074
QY	1024	ACAGTGCCTTATTTAGTAAAGCTGTGAATGATATAAAGAACTGTCAAACTATTACCAC	1083
Db	1075	ACTGTGCTCTTATTTAGTAAAGCTGTGAATGATATAAAGAACTGTCAAGCATTTACCAC	1134
QY	1084	GTGCATACAAATGCTGAGAACAAATATACCTGGCAGAAACTACTGTTTGTGATTTCCAT	1143
Db	1135	GTGCATACAAATGCTGAGAAATATAATACCTGGCTGAAACTACTGTTTGTGATTTCCAT	1194
QY	1144	CCAAAGCTTATTCATCAACACAAATTCAGCAGGCATGATCACAGGCTCGGCCAC	1203
Db	1195	CCAAAGCTTATTCATCAACACAAATTCAGCAGGCATGATCACAGGCTCGGCCAC	1254
QY	1204	CCTGTGTCAACAAAGGCGCAAGTCCCGACTCTGTGCCCTGGGAAATGGAATCTGG	1263
Db	1255	CCAGTGTCAACAAAGGCGCAAGTCCCGGTGCTGTGGCTCTGGGAAGTGGAAATTTGG	1314
QY	1264	GAACGTAAAGAGAGAGATTTACCTGTTGAAGAGCTGGGAAGTGGCCAGTTTGGAGTG	1323
Db	1315	GAACGTAAAGAGAGAGATTTACCTGTTGAAGAGCTGGGCAATGGCCAGTTTGGAGTG	1374
QY	1324	GTCCAGCTGGGCAAGTGGGAAGGCGAGTATGATGTTGCTGTTAAGATCATCAAGAGGCG	1383
Db	1375	GTCCAGCTGGGCGAGTGGGAAGGCGAATATGATGTTGGCTGTAAAGATGATCAAGAGGCT	1434
QY	1384	TCCATGTCAAGAGATGAATTTCTTTCAGGAGGCCAGACTATGATGAAACTCAGCCATCCC	1443
Db	1435	GCCATGTCAAGAGATGAATTTCTTTCAGGAGGCCAGACCATGATGAAACTCAGCCATCCC	1494
QY	1444	AAGCTGGTTAAATTTCTATGGAGTGTGTTCAAGAGNAATACCCATATACATAGTACTGAA	1503
Db	1495	AAGCTGGTTAAATTTCTACGAGTATGCTCAAGAAATACCCCATCTATATAGTACTGAG	1554
QY	1504	TATATAAGCAATGCTGCTTCTGAAATTAACCTGAGGAGTCAAGGAAAGAGCTTGAACCT	1563
Db	1555	TATATAAGCAATGCTGCTTCTGAAATTAACCTGAGGAGTCAAGGAAAGAGCTGAAAGT	1614
QY	1564	TCCAGCTCTTAGAAATTTCTAGCATGCTGTGTAAGGCATGGCCCTTCTTGGAGAGTCAAC	1623
Db	1615	TGCCAGCTCTTAGAAATTTCTATGATGCTGTGTAAGGCATGGCCCTTCTTGGAGAGCAT	1674
QY	1624	CAATTATACACCCGGACTTGGCTGCTGTAACCTGCTTGGTGACAGAGATCTCTGTGTG	1683
Db	1675	CAGTTATACATACCGAGATTTGGCTGCTCGAACTGTTTGGTGACAGTATCTCTCTGTG	1734
QY	1684	AAAGTATCTGACTTTTGGAAATGACAGAGTATGTTCTTTGATGACACAGTATGTCAGTCT	1743
Db	1735	AAAGTCTCAGACTTTTGGAAATGACAGAGATATGCTTTGATGATCAGTATGTCAGTCT	1794
QY	1744	GGAACAAAGTTTCCAGTCAAGTGGTCAGCTCCAGAGGTTGTTTCATTACTTCAAAATCACG	1803
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QY	1804	AGCAAGTCAAGAGTATGGGCAATTTGGATCCCTGATGCTGGAGCTGTTACGCTGGGAG	1863
Db	1855	AGCAAGTCAAGAGTATGGGCAATTTGGATCCCTGATGCTGGAGCTGTTTAGTCTAGGAG	1914
QY	1864	CAGCCCTATGACTTGTATGACAACTCCAGGTGGTTCTGAAGTCTCCAGAGGCCACAGG	1923
Db	1915	CAGCCCTATGACTTATATGATTAACCTCCAGGTGGTTCTGAAGTCTCCAGAGGCCACAG	1974
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Db	1975	CTCTACCGGCCCTGCTGCGATCGGACACCATCTACAGATCATGATGATGCTGCTGGCAT	2034
QY	1984	GAGCTTCCAGAAAGCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2043
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QY	2044	GAAAAAGCAACGATTTAGAGGAAATTTAGGAGTCTGATGAAGATTAAGATTAAGATTA	2103
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QY	2104	GCCAGCATTTTCATTTTAAAGAAAGTGAAGGCAATTAAGTAAATTTTGTAGTCTGTTT	2163
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QY	2391	--TTATTTGCTATGCTCACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2441
Db	2452	AAAAAATTTGGCAGTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2504
RESULT 2			
AK036707			
DEFINITION			
Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830165F06 product:BMX non-receptor tyrosine kinase, full insert sequence.			
ACCESSION			
AK036707.1 GI:26331623			
VERSION			
HTC; CAP trapper.			
KEYWORDS			
Mus musculus (house mouse)			
SOURCE			
Mus musculus			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
REFERENCE			
1 Carninci, P. and Hayashizaki, Y.			
AUTHORS			
TITLE			
High-efficiency full-length cDNA cloning			

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Meth. Enzymol. 303, 19-44 (1999)

99279253
10349636

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

20493374
11042159

JOURNAL
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AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

20530913
11076861

JOURNAL
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Katsuda, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staehli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, F., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., De Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660
11217851

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

6 (bases 1 to 2864)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp).

COMMENT

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://location.gsc.riken.go.jp/>

FEATURES
source

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/mol_type="mRNA"
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CDS

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polyA_site
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ORIGIN
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Qy 260 GACAGTACCCATTTTCAGATGCTGTATTAAGATGGGCTTCTCTATGATGATGATGATG 319
Db 241 GACAGTACCCATTTTCAGATGCTGTATTAAGATGGGCTTCTCTATGATGATGATGATG 300

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12716 row: m column: 21
High quality sequence stop: 644.
Location/Qualifiers
1. .986

FEATURES
source

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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
306 a 193 c 246 g 240 t 1 others

BASE COUNT 306 a 193 c 246 g 240 t 1 others
ORIGIN

Query Match 30.1%; Score 739.2; DB 12; Length 986;
Best Local Similarity 98.5%; Pred. No. 3.8e-138;
Matches 778; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

Qy 782 AAGTAGCAGCAGCAGTGAAGATGTTGCAAGCAGTAAACCAAAAGAAAGAAATGTGAATC 841
Db 7 AGAGTAGCAGCAGCAGTGAAGATGTTGCAAGCAGTAAACCAAAAGAAAGAAATGTGAATC 66
Qy 842 ACACCCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAAGAGGAAA 901
Db 67 ACACCCTCAAGATTTTCATGGGAATTCCTGAGTCAAGTTCATCTGAAGAAGAGGAAA 126
Qy 902 ACCTGGATGATATGACTGTTTCTGTTACATCTCCAGATCAATCTCAACAGTTAC 961
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RESULT 5
BQ878627

LOCUS BQ878627 830 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8124174 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6178136 5', mRNA sequence.

ACCESSION BQ878627
VERSION BQ878627.1 GI:22270635
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 830)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13557 row: d column: 09
High quality sequence stop: 707.
Location/Qualifiers
1. .830

FEATURES
source

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/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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5'-CAGTGTCTAGATCGCAGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 284 a 189 c 181 g 176 t
ORIGIN

Query Match 29.8%; Score 732.8; DB 13; Length 830;
Best Local Similarity 99.6%; Pred. No. 7.2e-137;
Matches 745; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DEFINITION AGENCOURT_7558402 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6046787
5', mRNA sequence.
ACCESSION  BQ229686
VERSION    BQ229686.1 GI:20411086
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS    Unpublished
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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BASE COUNT 296 a 184 c 183 g 193 t
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Db 802 CAGGGGAAA 810
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DEFINITION AGENCOURT_7560916 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6054864
5', mRNA sequence.
ACCESSION  BQ226991
VERSION    BQ226991.1 GI:20408391
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS    Unpublished
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13314 row: d column: 01
            High quality sequence stop: 703.
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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_72"
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                Average insert size 2 kb. Library constructed by Life
                Technologies."
BASE COUNT 294 a 196 c 196 g 198 t
ORIGIN
Query Match      27.8%; Score 683; DB 13; Length 890;
Best Local Similarity 99.3%; Pred. No. 7.5e-127;
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 QY 1770 AGCTCCAGAGTGTTTCTATTACTTCAATACAGCAGCAAGTCAACAGTATGGCATTTGG 1829
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 QY 1830 GATCCTGATGTGGGA 1844
 Db 29 GATCCTAATGTTAGA 15

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 ACCESSION BQ350538
 VERSION BQ350538.1 GI:21014594
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 651)
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3st2-RC3-HT0622-130400-022-f06&tl=2000-04-13&tl=1>)
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 /notes="Organ: head, neck; Vector: puc18; Site: 1: SmaI;
 Site: 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 167 a 176 c 130 g 178 t
 BASE COUNT 167 a 176 c 130 g 178 t
 ORIGIN

Query Match 25.0%; Score 614.4; DB 13; Length 651;
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 Matches 640; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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 QY 1314 GTTTGGAGTGTGCCAGCTGGGCAAGTGGAAAGGGGAGTATGATTTGCTGTTAAAGATGAT 1373
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 Db 471 CAAGGAGGGCTCCATGTCTCAGAAAGATGAATTTTTCAGGAGGCCAGAGCTATGATGAACT 412
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 QY 1614 GGAGAGTCACCAATTCATACACCGGAGTGTGCTGCTCGTAACTGCTGGTGGACAGAGA 1673
 Db 231 GGAGAGTCACCAATTCATACACCGGAGTGTGCTGCTCGTAACTGCTGGTGGACAGAGA 172
 QY 1674 TCTGTGCTGAAAGTATCTGACTTTGGAATGACAGAGTATGTTCTTGATGACCAAGTATGT 1733
 Db 171 TCTGTGCTGAAAGTATCTGACTTTGGAATGACAGAGTATGTTCTTGATGACCAAGTATGT 112
 QY 1734 CAGTTTCAGTCGGAACAAAGTTTCCAGTCAAGTGGTCCAGAGTGTCTTCATTACTT 1793
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 QY 1794 CAATATACAGCAGCAAGTCAAGTATGGGCATTTGGGATCCCTGATGTG 1841
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 ACCESSION BQ350352
 VERSION BQ350352.1 GI:21014408
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 628)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&ct2=RC3-HT0622-010400-021-b05&t3=2000-04-01&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 537.

FEATURES

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 /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 185 a 132 c 154 g 157 t
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 QY 1130 GTTTGATTCATTCCAAAGCTTATTCATTATCATCAACAAATTCAGAGGCATGATCA 1189
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 QY 1190 CAGGCTCCGCCACCTGCTCAACAGGCCACAGGTCGCCGACTCTGTGCCCTGG 1249
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 DB 541 TTCTTGAGAGTACCAATTCATACCGGACTTGGCTGCTCTTAAGTCTTGGTGGAC 600
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RESULT 12

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 VERSION BQ350539.1
 KEYWORDS GI:21014595
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 688)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&ct2=RC3-HT0622-130400-022-g06&t3=2000-04-13&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 633.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="HT0622"
 /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 173 a 181 c 141 g 192 t
 ORIGIN
 Query Match 24.1%; Score 592.2; DB 13; Length 688;
 Best Local Similarity 98.3%; Pred. No. 1.3e-108;
 Matches 619; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
 QY 1200 CCACCTCTGTCAACAAAGGCCAACAGTCCCTCCCTCTGTGTCTCCCTGGAAATGGAA 1259
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DB |||||||
QY 417 TCCCAAGCTGGTTAAATCTTATGAGTGTGTTCAAGGAATACCCCATATACATAGTGAC 358
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QY 1500 TGAATATATAGCAATGCTGCTTCTGCTGAATACCTGAGGAGTCACGGAAGGACTTGA 1559
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ACCESSION AK080038.1 GI:26348342
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REFERENCE 1
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          Meth. Enzymol. 303, 19-44 (1999)
          92279253
          PUBMED 10349636
REFERENCE 2
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          Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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          prepare full-length cDNA libraries for rapid discovery of new genes
          Genome Res. 10 (10), 1617-1630 (2000)
          20499374
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          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
          Konno, H., Akiyama, J., Nishi, K., Kitzunai, T., Tashiro, H., Itoh, M.,
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          Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
          RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer
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          PUBMED 11076861
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21085660
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5 The FANTOM Consortium and the RIKEN Genome Exploration Research
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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COMMENT

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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SOURCE
ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
10737800
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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